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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:51 ; Search time 31 Seconds
(without alignments)
2040.776 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002
Sequence: 1 MAAYVQPPHPPGPHGCV.....EVFITEPQSNHPQWLE 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppaa/PCF_NEW_PUB.pep:*
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18: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2002	100.0	343 10 US-09-934-706-1	Sequence 1, App1
2	1999	99.9	400 10 US-09-934-706-5	Sequence 5, App1
3	1999	99.9	501 10 US-09-934-706-4	Sequence 4, App1
4	1988	99.3	2320 12 US-10-279-733-8	Sequence 8, App1
5	1988	99.3	2355 12 US-10-144-194A-104	Sequence 104, App
6	1984	99.1	2386 11 US-09-961-403-1	Sequence 1, App1
7	1978	98.8	2328 15 US-10-171-311-64	Sequence 64, App1
8	610	30.5	463 12 US-10-144-194A-52	Sequence 52, App1
9	382.5	19.1	660 9 US-09-801-196-35	Sequence 35, App1
10	382.5	19.1	660 12 US-10-153-185-14	Sequence 14, App1
11	382.5	19.1	660 12 US-10-301-822-125	Sequence 125, App
12	382.5	19.1	660 12 US-10-219-561-14	Sequence 14, App1
13	382.5	19.1	660 12 US-10-131-985-25	Sequence 25, App1
14	382.5	19.1	660 15 US-10-219-329-14	Sequence 14, App1
15	382.5	19.1	663 12 US-10-115-223-30	Sequence 30, App1

16	380	19.0	429 12 US-10-115-223-45	Sequence 45, App1
17	374	18.7	707 9 US-09-801-196-36	Sequence 36, App1
18	374	18.7	707 12 US-10-301-822-132	Sequence 132, App
19	374	18.7	707 12 US-10-131-985-33	Sequence 33, App1
20	374	18.7	707 15 US-10-171-311-142	Sequence 142, App1
21	356.5	17.8	259 11 US-09-940-235-4	Sequence 4, App1
22	242	12.1	164 9 US-09-925-301-1270	Sequence 1270, App
23	235.5	11.8	793 15 US-10-171-311-62	Sequence 62, App1
24	229	11.4	231 9 US-09-925-302-548	Sequence 548, App
25	205	10.2	57 9 US-09-864-761-40316	Sequence 40316, A
26	193.5	9.7	1479 15 US-10-015-218-1738	Sequence 1738, App
27	193.5	9.7	1479 15 US-10-015-218-1739	Sequence 1739, App
28	193	9.6	1456 10 US-09-870-759-95	Sequence 95, App1
29	193	9.6	1456 12 US-09-751-708A-95	Sequence 115, App1
30	170	8.5	301 9 US-09-989-723-115	Sequence 115, App
31	170	8.5	301 9 US-09-989-723-115	Sequence 115, App
32	170	8.5	301 9 US-09-989-727-115	Sequence 115, App
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34	170	8.5	301 10 US-09-989-731-115	Sequence 115, App
35	170	8.5	301 10 US-09-989-733-115	Sequence 115, App
36	170	8.5	301 10 US-09-991-072-115	Sequence 115, App
37	170	8.5	301 10 US-09-990-442-115	Sequence 115, App
38	170	8.5	301 10 US-09-991-163-115	Sequence 115, App
39	170	8.5	301 10 US-09-993-604-115	Sequence 115, App
40	170	8.5	301 10 US-09-990-456-115	Sequence 115, App
41	170	8.5	301 10 US-09-989-721-115	Sequence 115, App
42	170	8.5	301 10 US-09-992-598-115	Sequence 115, App
43	170	8.5	301 10 US-09-989-293A-115	Sequence 115, App
44	170	8.5	301 10 US-09-989-735-115	Sequence 115, App
45	170	8.5	301 10 US-09-990-444-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-09-934-706-1
; Sequence 1, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Tectum Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified Human
; OTHER INFORMATION: Fibronectin Collagen-Binding Domain
; NAME/KEY: INIT_MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2..341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: CONFLICT
; LOCATION: (69)
; NAME/KEY: CONFLICT
; LOCATION: (125)
; US-09-934-706-1

Query Match 100.0% ; Score 2002; DB 10; Length 343;
Best Local Similarity 100.0% ; Pred No. 6.6e-179;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPGPHGCVTDSGVVYVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQ 60
Db 1 MAAYVQPPHPPGPHGCVTDSGVVYVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQ 60

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QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
QY 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
DB 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
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RESULT 2

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US-09-934-706-5
; Sequence 5, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; OTHER INFORMATION: Domain and Human Epidermal Growth Factor
; NAME/KEY: INIT _MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note="enterokinase recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(400)
; OTHER INFORMATION: /note="human epidermal growth factor"
US-09-934-706-5
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Query Match 99.9%; Score 1999; DB 10; Length 400;
Best Local Similarity 99.7%; Pred. No.1.5e-178;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
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DB 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
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RESULT 3

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US-09-934-706-4
; Sequence 4, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; OTHER INFORMATION: Domain and Human Basic Fibroblast Growth Factor
; NAME/KEY: INIT _MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note="enterokinase recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(501)
; OTHER INFORMATION: /note="human fibroblast growth factor"
US-09-934-706-4
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Query Match 99.9%; Score 1999; DB 10; Length 501;
Best Local Similarity 99.7%; Pred. No.2e-178;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
DB 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNVEODQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCSTSEGRDNMKWCTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
DB 181 CTTEGVMYRIGDQMDKQHDGMHMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVNVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCFGQGRGRWKCDPVDCODSEFTGYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPIDMLE 343
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RESULT 4

US-10-279-733-8
Sequence 8, Application US/10279733
Publication No. US20030194400A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Liu, Cheng
APPLICANT: Edgington, Thomas, S.
TITLE OF INVENTION: Targeted Thrombostasis
FILE REFERENCE: 1361.016W01
CURRENT APPLICATION NUMBER: US/10/279,733
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 60/336331
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 2320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-279-733-8

Query Match 99.3%; Score 1988; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 1.4e-176;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 256 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 315
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 121
DB 316 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 375
QY 122 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 181
DB 376 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 435
QY 182 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 241
DB 436 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 495
QY 242 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 301
DB 496 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 555
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIOW 341
DB 556 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIOW 595

RESULT 5

US-10-144-194A-104
Sequence 104, Application US/10144194A
Publication No. US20030215809A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.0
SEQ ID NO 104
LENGTH: 2355
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-194A-104

Query Match 99.3%; Score 1988; DB 12; Length 2355;
Best Local Similarity 100.0%; Pred. No. 1.4e-176;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 121
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 410
QY 122 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 181
DB 411 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 470
QY 182 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 241
DB 471 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 530
QY 242 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 301
DB 531 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 590
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIOW 630

RESULT 6

US-09-961-403-1
Sequence 1, Application US/09961403
Publication No. US2003007589A1
GENERAL INFORMATION:
APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2386
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-1

Query Match 99.1%; Score 1984; DB 11; Length 2386;
Best Local Similarity 99.7%; Pred. No. 3.3e-176;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAYYQPPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 121
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEQDOKYFSCDHTVLVQT 410
QY 122 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 181
DB 411 RGNNSGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADADOKFGFCPMAAHEIC 470
QY 182 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 241
DB 471 TTNEGVMYRIGDQMDQOHMGHMRCTCVNGRGEWTCIAYSQLRQCIYDDITVYVNDT 530
QY 242 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 301
DB 531 FHKRHEGHMLNCTCGGGRGWKCDPVDCODSEGTFTFYQIGDSMEKYVHGVRVYCYCY 590

Db 531 FHKEHBEHMLNCTCFGGGRGKMDPVDCQDSEGTFTFYIGDSWEKXVHGVRVQCYCY 590
Qy 302 GRGIGEMHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIQM 341
Db 591 GRGIGEMHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIQM 630

RESULT 7

US-10-171-311-64
; Sequence 64, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 2328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-64

Query Match 98.8%; Score 1978; DB 15; Length 2328;
Best Local Similarity 99.4%; Pred. No. 1.2e-175;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AAVYQPPHPPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
Db 264 AAVYQPPHPPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 323
Qy 62 YGNSNGEPCVLPPTNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 121
Db 324 YGNSNGEPCVLPPTNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 383
Qy 122 RGSNSNALCHFPFLYNNHNTDCTSEGRBDNMKCGTTONVYDADQKGFCEMAHEITC 181
Db 384 QGGSNSNALCHFPFLYNNHNTDCTSEGRBDNMKCGTTONVYDADQKGFCEMAHEITC 443
Qy 182 TTNGVWVRIDQMDKQDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYDITVNVDT 241
Db 444 TTNGVWVRIDQMDKQDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYDITVNVDT 503
Qy 242 FHKEHBEHMLNCTCFGGGRGKMDPVDCQDSEGTFTFYIGDSWEKXVHGVRVQCYCY 301
Db 504 FHKEHBEHMLNCTCFGGGRGKMDPVDCQDSEGTFTFYIGDSWEKXVHGVRVQCYCY 563
Qy 302 GRGIGEMHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIQM 341
Db 564 GRGIGEMHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIQM 603

RESULT 8
US-10-144-194A-52
; Sequence 52, Application US/10144194A
; Publication No. US20030215809A1

; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-52

Query Match 30.5%; Score 610; DB 12; Length 463;
Best Local Similarity 99.1%; Pred. No. 1.3e-48;
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAVYQPPHPPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
Db 327 AAVYQPPHPPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 386
Qy 62 YGNSNGEPCVLPPTNGRTFTYSCCTEGRODGHLMCSTTSNYEDQK 108
Db 387 YGNSNGEPCVLPPTNGRTFTYSCCTEGRODGHLMCSTTSNYEDQK 433

RESULT 9

US-09-801-196-35
; Sequence 35, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-35

Query Match 19.1%; Score 382.5; DB 9; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

Qy 55 ETAVTQTYGNSNGEPCVLPPTNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTD 114
Db 217 EGQVVRKYNGADGEYCKFPFLFNGKEYNSCTDGRSDGLMCSITVNFEXDKGYGFC-P 275
Qy 115 HTVIVQIRGNSNALCHFPFLYNNHNTDCTSEGRBDNMKCGTTONVYDADQKGFCEPM 174
Db 276 HEALF-TWGNVABEQPKCFPPFRFGTSYDSCCTEGRTDGYRWCGTIEDYDRDKKYGFCPE 334
Qy 175 AAHEICTTNEGV-----MYRIGDQMDKQDMGMMRCTCVNGRGEMTCIA--YSQLR 226
Db 335 TMSVTVGNSBGAACVFPFTFLNGKYS-----CTAGNSDGMWCAATTANYVDDDR 385
Qy 227 DQCIYDITVNVDTFHKEHBEHML 252
Db 386 KWGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 10
US-10-153-185-14
; Sequence 14, Application US/10153185

GENERAL INFORMATION:
APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT FILING DATE: 2002-04-25
PRIORITY FILING DATE: 2002-04-25
PRIORITY FILING DATE: 2000-11-30
PRIORITY FILING DATE: 2000-11-30
PRIORITY FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-25

Query Match 19.1%; Score 382.5; DB 12; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTYGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114
DB 217 EGQVVRVYKGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFCPM 174
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFCPM 174
DB 276 HEALF-TWGNABEQPCPKFPFRFGTSDCTTEGRTDGYWCGTTEDYDRDKKYGFCPE 334
QY 175 AAHEICTTNGV-----MYRIGDQMDKOHMGHMRCTCVNGRGWTCIA---YSQLR 226
DB 335 TAMSTVGNSGACVCPFPFTFLGNKYES-----CTSGRSDGKXWCATTANYDDDR 385
QY 227 DQCIYDITVYVNDTFHKKRHEGHML 252
DB 386 KWGFCPDQGYSL--FLVAHAHFGHAM 409

RESULT 14
US-10-219-329-14
Sequence 14, Application US/10219329
Publication No. US20030096757A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Weart, Ilona F.
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT FILING DATE: 2002-08-15
PRIORITY FILING DATE: 2002-08-15
PRIORITY FILING DATE: 2001-12-21
PRIORITY FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-329-14

Query Match 19.1%; Score 382.5; DB 15; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
QY 55 ETAVTQTYGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114

DB 217 EGQVVRVYKGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFC-P 275
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFCPM 174
DB 276 HEALF-TWGNABEQPCPKFPFRFGTSDCTTEGRTDGYWCGTTEDYDRDKKYGFCPE 334
QY 175 AAHEICTTNGV-----MYRIGDQMDKOHMGHMRCTCVNGRGWTCIA---YSQLR 226
DB 335 TAMSTVGNSGACVCPFPFTFLGNKYES-----CTSGRSDGKXWCATTANYDDDR 385
QY 227 DQCIYDITVYVNDTFHKKRHEGHML 252
DB 386 KWGFCPDQGYSL--FLVAHAHFGHAM 409

RESULT 15
US-10-115-223-30
Sequence 30, Application US/10115223
Publication No. US20030176334A1
GENERAL INFORMATION:
APPLICANT: Cheresch, David A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
FILE REFERENCE: MER00495
CURRENT FILING DATE: 2002-04-02
PRIORITY FILING DATE: 2002-04-02
PRIORITY FILING DATE: 1999-03-23
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 663
TYPE: PRT
ORGANISM: Gallus gallus
US-10-115-223-30

Query Match 19.1%; Score 382.5; DB 12; Length 663;
Best Local Similarity 37.0%; Pred. No. 3.6e-27;
Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;

QY 55 ETAVTQTYGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114
DB 214 EGQVVRVYKGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFCPH 273
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTQNYADOKFGFCPM 174
DB 274 ESLE-TWGNABEQPCPKFPFRFGTSDCTTEGRTDGYWCGTTEDYDRDKKYGFCPE 331
QY 175 AAHEICTTNGV-----MYRIGDQMDKOHMGHMRCTCVNGRGWTCIA---YSQLR 226
DB 332 TAMSTVGNSGACVCPFPFTFLGNKYDS-----CTSGRSDGKXWCATTANYDDDR 382
QY 229 ----CIYDITVYVNDTFHKKRHEGHML 252
DB 383 KWGFC--PDQGYSL--FLVAHAHFGHAM 406

Search completed: November 28, 2003, 15:03:26
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 / Search time 21 Seconds
(without alignments)
691.077 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002
Sequence: 1 MAAYVQPPHPQPPYHCV.....EVFITETPQNSHPQWLE 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	98.9	2386	2	US-09-016-366A-12
2	1978	98.8	2446	2	PCT-US-51-356-2
3	1978	98.8	2446	5	PCT-US93-12687-2
4	1973	98.6	2337	6	545158-1
5	1971	98.5	2334	1	US-08-283-857-1
6	1971	98.5	2334	5	PCT-US95-09819-1
7	1959	97.9	2231	1	US-08-153-799-16
8	382.5	19.1	631	3	US-08-448-489-17
9	382.5	19.1	660	3	US-08-704-711A-18
10	382.5	19.1	660	4	US-09-521-220-18
11	382.5	19.1	660	4	US-09-381-104-19
12	382.5	19.1	663	4	US-09-194-468A-30
13	380	19.0	429	4	US-09-194-468A-45
14	374	18.7	707	3	US-08-704-711A-19
15	374	18.7	707	4	US-09-521-220-19
16	374	18.7	707	4	US-09-391-104-20
17	374	18.7	708	3	US-08-448-489-16
18	371	18.5	65	2	US-08-982-597A-19
19	371	18.5	65	3	US-09-136-218-19
20	348	17.4	60	3	US-08-982-597A-18
21	348	17.4	60	3	US-09-136-218-18
22	290	14.5	48	2	US-08-982-597A-22
23	290	14.5	48	3	US-09-136-218-22
24	278	13.9	48	2	US-08-982-597A-20
25	278	13.9	48	3	US-09-136-218-20
26	258	12.9	43	2	US-08-982-597A-21
27	258	12.9	43	3	US-09-136-218-21

28	243	12.1	474	2	US-08-836-854-9	Sequence 9, Appl
29	239.5	12.0	422	2	US-08-836-854-12	Sequence 12, Appl
30	232	11.6	188	1	US-08-142-448B-14	Sequence 14, Appl
31	206	10.3	37	2	US-08-982-597A-17	Sequence 17, Appl
32	206	10.3	37	3	US-09-136-218-17	Sequence 17, Appl
33	202	10.1	1455	3	US-08-840-062-5	Sequence 5, Appl
34	195.5	9.8	1463	1	US-08-220-603A-11	Sequence 11, Appl
35	193.5	9.7	1479	3	US-08-840-062-4	Sequence 4, Appl
36	187	9.3	1479	3	US-08-840-062-2	Sequence 2, Appl
37	180.5	9.0	1487	3	US-08-840-062-7	Sequence 7, Appl
38	170	8.5	301	4	US-09-996-243-115	Sequence 115, App
39	170	8.5	655	1	US-08-148-910-12	Sequence 12, Appl
40	170	8.5	655	1	US-08-448-937A-12	Sequence 12, Appl
41	143	7.1	1722	4	US-09-194-612A-1	Sequence 1, Appl
42	140.5	7.0	1449	3	US-08-840-062-6	Sequence 6, Appl
43	140.5	7.0	1723	4	US-09-194-612A-31	Sequence 31, Appl
44	130	6.5	24	2	US-08-982-597A-23	Sequence 23, Appl
45	130	6.5	24	3	US-09-136-218-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-016-366A-12
Sequence 12, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2386 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-016-366A-12

Query Match

Best Local Similarity

Matches 338; Conservative

98.9%; Score 1979; DB 2; Length 2386;

Pred. No. 9,4e-175;

Indels 0; Gaps 0;

Mismatches 1;

1;

QY 2 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGPCVLPPTVNGRTFYSCCTEGRODGHLMCSTTSYEDDOKYSFCTDHTVLVQT 121
DB 351 YGNSNGPCVLPPTVNGRTFYSCCTEGRODGHLMCSTTSYEDDOKYSFCTDHTVLVQT 410
QY 122 RGNNSGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHEBIC 181
DB 411 QGNSNGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHEBIC 470
QY 182 TTNGVWYRIDDQWDKQHDGMHMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVNDT 241
DB 471 TTNGVWYRIDDQWDKQHDGMHMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVNDT 530
QY 242 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVRYQCY 301
DB 531 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVRYQCY 590
QY 302 GRGIGEMHCQPLQTYPPSSSGPEVEFTTETPSQPNSHPIQW 341
DB 591 GRGIGEMHCQPLQTYPPSSSGPEVEFTTETPSQPNSHPIQW 630

RESULT 2

US-08-551-356-2
; Sequence 2, Application US/08551356
; Patent No. 5830700
; GENERAL INFORMATION:
; APPLICANT: Iran, Meher H.
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,356
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,762
; FILING DATE:
; APPLICATION NUMBER: US/07/998,271
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Holly, Julie A
; REGISTRATION NUMBER: 33-246
; REFERENCE/DOCKET NUMBER: 92-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-551-356-2

Query Match 98.8%; Score 1978; DB 2; Length 2446;
Best Local Similarity 99.4%; Pred. No. 1,2e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGPCVLPPTVNGRTFYSCCTEGRODGHLMCSTTSYEDDOKYSFCTDHTVLVQT 121
DB 351 YGNSNGPCVLPPTVNGRTFYSCCTEGRODGHLMCSTTSYEDDOKYSFCTDHTVLVQT 410
QY 122 RGNNSGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHEBIC 181
DB 411 QGNSNGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHEBIC 470
QY 182 TTNGVWYRIDDQWDKQHDGMHMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVNDT 241
DB 471 TTNGVWYRIDDQWDKQHDGMHMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVNDT 530
QY 242 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVRYQCY 301
DB 531 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVRYQCY 590
QY 302 GRGIGEMHCQPLQTYPPSSSGPEVEFTTETPSQPNSHPIQW 341
DB 591 GRGIGEMHCQPLQTYPPSSSGPEVEFTTETPSQPNSHPIQW 630

RESULT 3

PCT-US93-12687-2
; Sequence 2, Application PC/TUS9312687
; GENERAL INFORMATION:
; APPLICANT: Iran, Meher H.
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12687
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/998,271
; FILING DATE: 31-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 92-26PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12687-2

Query Match 98.8%; Score 1978; DB 5; Length 2446;
Best Local Similarity 99.4%; Pred. No. 1,2e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350

QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 121
DB 351 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 410
QY 122 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
DB 411 QGNSNGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 470
QY 182 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 241
DB 471 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 530
QY 242 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 301
DB 531 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 590
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 341
DB 591 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 630

RESULT 4
5455158-1
PATENT NO. 5455158
APPLICANT: VOGEL, TIKVA, LEVANON, AVIGDOR, WEBER, MOSHE M.;
GUY, RACHEL, PANET, AMOS
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
USERS AND METHODS OF PRODUCING SAME
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 526,397
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: 345,952
FILING DATE: 28-APR-1989
APPLICATION NUMBER: 291,951
FILING DATE: 29-DEC-1988
SEQ ID NO: 1
LENGTH: 2327
5455158-1

Query Match 98.6%; Score 1973; DB 6; Length 2327;
Best Local Similarity 99.1%; Pred. No. 3.3e-174;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAYYQPHQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 263 AAYYQPHQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 322
QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 121
DB 323 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 382
QY 122 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
DB 383 QGNSNGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 442
QY 182 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 241
DB 443 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 502
QY 242 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 301
DB 503 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 562
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 341
DB 563 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 602

RESULT 5
US-08-283-857-1
Sequence 1, Application US/08283857
Patent No. 5792742
GENERAL INFORMATION:
APPLICANT: GOLD, Leslie I.
APPLICANT: ROSTAGNO, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J. FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/714,134
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-283-857-1

Query Match 98.5%; Score 1971; DB 1; Length 2324;
Best Local Similarity 99.1%; Pred. No. 5e-174;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAYYQPHQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 260 AAYYQPHQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 319
QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 121
DB 320 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSSTNSYEDOKYSECTDHTVLVOT 379
QY 122 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
DB 380 QGNSNGALCHFPFLYNNHNYTDCSTSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 439
QY 182 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 241
DB 440 TTNEGVYRIGDQWDKQDHGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDDITTYVNDT 499
QY 242 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 301
DB 500 FHKRHEBGMHNLCTCFQGRGRWKCDPVDCODESETGFYQIGDSWEKYHGVRYOCYCY 559
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 341

Db 560 GRGIGEMHCOPLOYYPSSSGPEVEFITETPSQPNSHPIQW 599

RESULT 6

PCT-US95-09819-1
Sequence 1, Application PC/TUS9509819

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA

TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09819

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,857

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: GOLD-1A PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2324 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-09819-1

Query Match 98.5%; Score 1971; DB 5; Length 2324;

Best Local Similarity 99.1%; Pred. No. 5e-174;

Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 AAVYQPPHPPPPYGHGCVTDSGVVYSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61

Db 260 AAVYQPPHPPPPYGHGCVTDSGVVYSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 319

QY 62 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDQKYSFCTDHTVLVQT 121

Db 320 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDQKYSFCTDHTVLVQT 379

QY 122 RGSNSNGALCHFPPLYNNTTDCSSGRRNMMKCGTTQYVDDQKGFCPMAAHEIC 181

Db 380 QGGSNSNGALCHFPPLYNNTTDCSSGRRNMMKCGTTQYVDDQKGFCPMAAHEIC 439

QY 182 TTNSGVWVRIGDDMDKDHMMRCCTGVNGRGFWTCIAVSQLRDQCTIVDDITVYVNT 241

Db 440 TTNSGVWVRIGDDMDKDHMMRCCTGVNGRGFWTCIAVSQLRDQCTIVDDITVYVNT 499

QY 242 FHKHSEGHMLNCTCFQGRGRWKCDPYDQCDSETGTFFYQIGDSWEKTVHGVAYQCYCY 301

Db 500 FHKHSEGHMLNCTCFQGRGRWKCDPYDQCDSETGTFFYQIGDSWEKTVHGVAYQCYCY 559

QY 302 GRGIGEMHCOPLOYYPSSSGPEVEFITETPSQPNSHPIQW 341

Db 560 GRGIGEMHCOPLOYYPSSSGPEVEFITETPSQPNSHPIQW 599

RESULT 7

US-08-153-799-16
Sequence 16, Application US/08153799

Patent No. 5766883

GENERAL INFORMATION:

APPLICANT: Ballance, David J

APPLICANT: Goodey, Andrew R

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: R Hain Swope, BOC Health Care Inc

STREET: 100 Mountain Avenue

CITY: Murray Hill

STATE: New Jersey

COUNTRY: USA

ZIP: 07974

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,799

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847975

FILING DATE: 06-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8909916.2

FILING DATE: 29-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB90/00650

FILING DATE: 26-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/775952

FILING DATE: 29-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Swope, R Hain

REGISTRATION NUMBER: 24864

REFERENCE/DOCKET NUMBER: 92H832

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 665 2400

TELEFAX: (908) 771 6159

TELEX: 219484

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Protein

LOCATION: 1..2231

OTHER INFORMATION: /note= "Human fibronectin"

US-08-153-799-16

Query Match 97.9%; Score 1959; DB 1; Length 2231;

Best Local Similarity 99.1%; Pred. No. 6.2e-173;

Matches 336; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 AAVYQPPHPPPPYGHGCVTDSGVVYSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61

Db 260 AAVYQPPHPPPPYGHGCVTDSGVVYSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 319

QY 62 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDQKYSFCTDHTVLVQT 121

Db 320 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEODKYSFCTDHTLVOT 379
QY 122 RGNNGALCHPEFLYNNHNYTDCTSEGRDNMKCGTTONYADOKFGFCPMAAHEBIC 181
Db 380 QGNSNGALCHPEFLYNNHNYTDCTSEGRDNMKCGTTONYADOKFGFCPMAAHEBIC 439
QY 182 TTNEGVMYRIGDOWDKOHDMGMMRCTCVNGRGEMWTCIAVSQLRDQCIYDITVNDT 241
Db 440 TTNEGVMYRIGDOWDKOHDMGMMRCTCVNGRGEMWTCIAVSQLRDQCIYDITVNDT 489
QY 242 FHKRHEGMLNCTCGGQGRMKCDPVQCCDSEGTGTFOIGDSWEKYVGVRYOCYCY 301
Db 500 FHKRHEGMLNCTCGGQGRMKCDPVQCCDSEGTGTFOIGDSWEKYVGVRYOCYCY 559
QY 302 GRGIGEMHCOPLQTPSSSGPVEFITEPSPNSHPIQ 340
Db 560 GRGIGEMHCOPLQTPSSSGPVEFITEPSPNSHPIQ 598

RESULT 8

US-08-448-489-17
Sequence 17, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 17
LENGTH: 631
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Known Member of
US-08-448-489-17

Query Match 19.1%; Score 382.5; DB 3; Length 631;
Best Local Similarity 38.3%; Pred. No. 2.9e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
QY 55 ETAVTQTYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEODKYSFCTD 114
Db 188 EGQVNVKYGNADEYCKPFLFNKGKYNSTCTDGRSDGFLMSTTYNFEKDGKYGFC-P 246
QY 115 HTVLVOTRGNNGALCHPEFLYNNHNYTDCTSEGRDNMKCGTTONYADOKFGFCPM 174
Db 247 HEALF-TMGNAAGOPCKPFRFGTSTYSDCTTEGRDGRMGCTTEDYDRDKYGCPE 305
QY 175 AAHEBICCTNEGV----MYRIGDOWDKOHDMGMMRCTCVNGRGEMWTCIA---YSQLR 226
Db 306 TASTYGNSEGAFCVPFFFLGNKYS-----CTSAGSDGKMKCATYANDDDR 356
QY 227 DQCIYDITVNDTFAKHEBGM 252
Db 357 KMGFCPDQGYSL--FLVAHEFGHAM 380

RESULT 9
US-08-704-711A-18
Sequence 18, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
METALLOPROTEASES, THEIR PRODUCTION AND USE

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-18

Query Match 19.1%; Score 382.5; DB 3; Length 660;
Best Local Similarity 38.3%; Pred. No. 3e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
QY 55 ETAVTQTYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEODKYSFCTD 114
Db 217 EGQVNVKYGNADEYCKPFLFNKGKYNSTCTDGRSDGFLMSTTYNFEKDGKYGFC-P 275
QY 115 HTVLVOTRGNNGALCHPEFLYNNHNYTDCTSEGRDNMKCGTTONYADOKFGFCPM 174
Db 276 HEALF-TMGNAAGOPCKPFRFGTSTYSDCTTEGRDGRMGCTTEDYDRDKYGCPE 334
QY 175 AAHEBICCTNEGV----MYRIGDOWDKOHDMGMMRCTCVNGRGEMWTCIA---YSQLR 226
Db 335 TASTYGNSEGAFCVPFFFLGNKYS-----CTSAGSDGKMKCATYANDDDR 385
QY 227 DQCIYDITVNDTFAKHEBGM 252
Db 386 KMGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 10
US-09-521-220-18
Sequence 18, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
METALLOPROTEASES, THEIR PRODUCTION AND USE
CORRESPONDENCE ADDRESS:

QY 175 AAHEICTTNEGV-----MYRIGDQMDKOHDMGMNRCCTCVGNGRGEMTCTIAYSQLRDO- 228
DB 332 TMSVTVGNSSEGAFCVPEPFIPLGNKYDS-----CTSGRNDGKLMWCASTSSVDDDR 382
QY 229 ----CIVDDITTVVNDTFKRRHEGML 252
DB 383 KMGFC--PDQGYSL--FLVAAHEFGHAM 406

RESULT 13

US-09-194-468A-45
; Sequence 45, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER00495
; CURRENT APPLICATION NUMBER: US/09/194,468A
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-45

Query Match 19.0%; Score 380; DB 4; Length 429;
Best Local Similarity 45.0%; Pred. No. 3e-27;
Matches 77; Conservative 20; Mismatches 56; Indels 18; Gaps 6;

QY 16 YGHCVTDSGVVSVGMQMLTKQGNKOMLCTCLAGNVSCQETAVTYQYGGNSNEPCVLPF 75
DB 13 YNSC-TDTG--RSDDGLMCSSTYVNFK---DKYGFCEPHEALF-TWGGNAECQPCPKFPF 64
QY 76 TNGRFTVSCCTEGRDGHLMCSTTSNYBODKYSFCTHTVTVQTRGNSNGLCH 135
DB 65 RFGGTSYDSTCTTGRTDGYWCGTTEBDYDKKYGFCPE--TMSVTVGNSSEGAFCVPEP 122
QY 136 LYNNHNYTDCSTSEGRDNMKCGTTONYADOKFGFCP-----MAAHE 178
DB 123 TFLGNKYESTSAGRSKGKWCATYANYYDDRKMGFCPDQGYSLFLVAAHE 173

RESULT 14

US-08-704-711A-19
; Sequence 19, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-704-711A-19

Query Match 18.7%; Score 374; DB 3; Length 707;
Best Local Similarity 40.1%; Pred. No. 2e-26;
Matches 77; Conservative 29; Mismatches 56; Indels 30; Gaps 7;

QY 16 YGHCVTDSGVVSVGMQMLTKQGNKOMLCTCLAGNVSCQETAVTYQYGGNSNEPCVLPF 75
DB 241 YSACTTDDG--SSDGLPMCSSTYVNFK---TDRFRCPSERLYTR--DGNADGKPCQFPF 292
QY 76 TNGRFTVSCCTEGRDGHLMCSTTSNYBODKYSFCTHTVTVQTRGNSNGLCH 132
DB 293 IFQGGYSYACTTGRDGRWCACTYANYPDKUFGCPTRADSTVW-----GGSAGBLCV 348
QY 133 FPLNNHNYTDCSTSEGRDNMKCGTTONYADOKFGFCP-----MAAHE----- 178
DB 349 FPFRTLKXSYSTSSGREGDGRMCACTISNPSDKMGFCPDQGYSLFLVAAHEFGHALG 408
QY 179 -EICTTNEGVY 189
DB 409 LDHSSVPEALMY 420

RESULT 15

US-09-521-220-19
; Sequence 19, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/521,220
FILING DATE: 06 May 2009

FILING DATE: 08-Mar-2000

CLASSIFICATION: <Unknown>
31-OCT-1994

21-OCT-1994
17-MAR-1994

17-MAR-1994
R APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,711

FILING DATE: <Unknown>

APPLICATION NUMBER: DE 4438838.1
FILING DATE: 31 OCT 1994

FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4408663 1

APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994

FILED DATE: 1/-MAR-1994

NAME: GRANADOS, Patricia

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26

COMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

ON FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids

LENGTH: 707 amino acid
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

ENCE DESCRIPTION: SEQ

-19

Query Match

Query Match	Score	DB 4	Length	707
18.78	374			

Best Local Similarity 40.1%; Pred. No. 2e-26;
Matches 77; Conservativeness 39; Mismatches 56; Indels 30; Cons 5

Matches	77;	conservative	29;	Mismatches	56;	Indels	30;	Gaps	7;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

```

QY      16 YGHCIVTDSGVVYVGMQMLTKQGNKQMLCTCLGNGVGSQCEATVPTQSGNSNGEVCVLPF 75
Db      241 YSACTTIDG---RBDGLPMCSSTAND---TDRFQFCSERLYLR--DGNADKRCQPPF 292
QY      76 TYNGRTFFYSCTTBGRDGHLMCSTTSNVEBQDKYSFC--TDHTVLVOTRGANGNGLCH 132
Db      293 IFQGGYSACTTIDGRSDGYRWACATTANYDRDLFGFCPTPADSTYM---GGSAGELCV 348
QY      133 FPEFLYNNHNTDCTSSGPRDNNMKCGCTONVYADQKFGFCP-----MAHE----- 178
Db      349 FPEFLGKEKYSTCTSGEGRDGHLMCATTSNFPDSDKMGFCPDQGSFLFLVAHHEFGHALG 408
QY      179 -EICTTNEGVMY 189
Db      409 LDHSSVPEALMY 420

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Search completed: November 28, 2003, 15:02:42
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 42 Seconds
(without alignments)
2107.430 Million cell updates/sec

Title: US-09-934-706-1
Perfect score: 2002
Sequence: 1 MAAYVQPPHQPYPYGHCV.....EVEFTTPSQNSHPICWLE 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1422	71.0	922	13	Q93405
3	1422	71.0	2478	13	Q93406
4	1190	59.4	205	4	Q9HAP3
5	1091	54.5	379	4	Q95610
6	750	37.5	141	13	Q90XQ2
7	405	20.2	679	13	Q98856
8	392	19.6	675	13	Q98856
9	391	19.5	690	13	Q98856
10	389.5	19.5	671	13	Q9W7L6
11	383.5	19.2	655	13	Q9W635
12	383.5	19.2	673	13	Q907B3
13	381.5	19.1	632	6	Q9N1P6
14	379.5	19.0	686	13	Q9DE15
15	378.5	18.9	661	6	Q95J74
16	378	18.9	707	4	Q8N725

17	377.5	18.9	674	13	Q98TC6	Q98TC6 cyprinus ca
18	374.5	18.7	385	6	Q9TUL8	Q9TUL8 equus caball
19	372.5	18.6	661	6	Q9GLE5	Q9GLE5 bos taurus
20	366	18.3	704	6	Q19130	Q19130 canis famill
21	365.5	18.3	657	13	Q9PTU7	Q9PTU7 oxyrias lat
22	360	18.0	656	13	Q8BUZ3	Q8BUZ3 xenopus lae
23	359.5	18.0	658	13	Q90YB4	Q90YB4 parailichthy
24	348	17.4	266	11	Q8C6J7	Q8C6J7 mus musculu
25	326	16.3	208	6	Q9XSD1	Q9XSD1 canis famill
26	317	15.8	324	6	Q9N282	Q9N282 bos taurus
27	316.5	15.8	111	6	Q95166	Q95166 canis famill
28	272.5	13.6	223	4	Q96RT0	Q96RT0 mus musculu
29	269.5	13.5	220	4	Q9H4C8	Q9H4C8 mus musculu
30	269.5	13.5	223	4	Q96H33	Q96H33 mus musculu
31	261	13.0	245	6	Q9GJ25	Q9GJ25 canis famill
32	261	13.0	261	6	Q9GJ26	Q9GJ26 canis famill
33	242.5	12.1	638	13	Q8AX63	Q8AX63 silurus aso
34	232.5	11.6	216	11	Q99XDO	Q99XDO mus musculu
35	232.5	11.6	810	11	Q8R3F3	Q8R3F3 mus musculu
36	217	10.8	351	6	Q02816	Q02816 oryctolagus
37	214	10.7	153	4	Q9H382	Q9H382 mus sapien
38	203	10.1	1326	4	Q13019	Q13019 mus sapien
39	203	10.1	1465	4	Q13018	Q13018 mus sapien
40	202	10.1	320	4	Q96KP8	Q96KP8 mus sapien
41	202	10.1	1456	11	Q61830	Q61830 mus musculu
42	199.5	10.0	320	6	Q95KV4	Q95KV4 bos taurus
43	195	9.7	653	11	Q8VCS4	Q8VCS4 mus musculu
44	194	9.7	2328	6	Q95MT9	Q95MT9 etineaceus e
45	193.5	9.7	1479	4	Q9Y5P9	Q9Y5P9 mus sapien

ALIGNMENTS

RESULT 1
ID Q81V18 PRELIMINARY; PRT; 657 AA.
AC Q81V18;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Migration stimulation factor FN70+.
GN FN.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schor S.L., Schor A.M., Kay R.A.;
RT "The sequence of MSF/FN70 + variant.",
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535086; CAD59389.1; -
SQ SEQUENCE 657 AA; 73752 MW; 8CA04E64486ABCD0 CRC64;

Query Match 99.3%; Score 1988; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 2e-179;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	AAAYOPPPHQPYPYGHCVTDGVSVMQMTQGNKQMLCTCIGNGVSCQETAVTQF 61
DB	291	AAAYOPPPHQPYPYGHCVTDGVSVMQMTQGNKQMLCTCIGNGVSCQETAVTQF 350
QY	62	YGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGLMCSITSNYEDQKSFCTDHTVLVQT 121
DB	351	YGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGLMCSITSNYEDQKSFCTDHTVLVQT 410
QY	122	RGNSNGALCHPFLVNNHNYTCTSEGRDNNKNGCTTQNTADQKFGCPAAAEETC 181
DB	411	RGNSNGALCHPFLVNNHNYTCTSEGRDNNKNGCTTQNTADQKFGCPAAAEETC 470
QY	182	TTREGVWYRIGDQMDKQHDGMHMRCTCVNGNGEWTCTAYSQLROCCIYDDITVAVNDT 241

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Db 471 TTNEGVWYRIDQNDKQHDMMKCTCTGNGRGEMTICIAVSQLRDQCIYDDITVYNDT 530
QY 242 FHKHREBGMNLNCTCFQGGGRMKCDPYDQOCDESETGYOIGDSWEKYVHGVYQCYC 301
Db 531 FHKHREBGMNLNCTCFQGGGRMKCDPYDQOCDESETGYOIGDSWEKYVHGVYQCYC 590
QY 302 GRGIGEMHCOPLOQTYPSSSGPVEVFITETPSQPNSHPIOW 341
Db 591 GRGIGEMHCOPLOQTYPSSSGPVEVFITETPSQPNSHPIOW 630

RESULT 2
ID 093405 PRELIMINARY; PRT; 922 AA.
AC 093405;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Fibroneclin.
GN FN1 OR FN2.
OC Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao O., Collodi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081127; AAC31941.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 9.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 2.
DR PRINTS; PR00013; FNTYPEII.
DR PRODOM; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 922 AA; 101814 MW; EF83E4CACBD0080 CRC64;

Query Match 71.0%; Score 1422; DB 13; Length 922;
Best Local Similarity 68.6%; Pred. No. 1e-125;
Matches 234; Conservative 48; Mismatches 57; Indels 2; Gaps 2;
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Db 587 YGNIGELSCBPQHSISGHRPVQVILISEAGNPNSHPIOW 627
RESULT 3
ID 093406 PRELIMINARY; PRT; 2478 AA.
AC 093406;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Fibroneclin.
GN FN1.
OC Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao O., Collodi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081128; AAC31947.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRODOM; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 2478 AA; 271652 MW; A03475C58385750 CRC64;

Query Match 71.0%; Score 1422; DB 13; Length 2478;
Best Local Similarity 68.6%; Pred. No. 3.3e-125;
Matches 234; Conservative 48; Mismatches 57; Indels 2; Gaps 2;
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ID Q9HAP3 PRELIMINARY; PRT; 205 AA.
AC Q9HAP3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Fibronection (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=55284965; PubMed=2992939;
RA Kornblith A.R., Umezawa K., Vide-Pedersen K., Baralle F.E.;
RT "primary structure of human fibronection: differential splicing may
RT generate at least 10 polypeptides from a single gene.";
RL EMBL J. 4:1755-1759 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Steffensen B., Martin P.A.;
RT "Fibronection collagen binding domain (modules I6, I11, I12, I17).";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF312399; AAG30571.1; -.
DR HSSP; P02751; 2FN2.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 2.
DR Pfam; PF00040; fn2; 2.
DR PRINTS; PR00012; FNTYPEII.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
FT NON_TER 1 50 S -> L (IN REF. 1).
FT CONFLICT 106 106 R -> Q (IN REF. 1).
FT NON_TER 205 205
SQ SEQUENCE 205 AA; 22947 MW; B423205B9B65F989 CRC64;

Query Match 59.4%; Score 1190; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GHCVTDSGVVSYVGMQLKTQGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPCVLPFT 76
DB 1 GHCVTDSGVVSYVGMQLKTQGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPCVLPFT 60

QY 77 YNRTFPTSCCTEGRDGHLMCSTTSNVEDOKYSFCTDHTVLVQTRGNSNGALCHPPEL 136
DB 61 YNRTFPTSCCTEGRDGHLMCSTTSNVEDOKYSFCTDHTVLVQTRGNSNGALCHPPEL 120

QY 137 YNNHNTYDCTSEGRDMMKMGCTTQNYADADOKFGFCPMAAHEICTTNEGVMYRIGDQMD 196
DB 121 YNNHNTYDCTSEGRDMMKMGCTTQNYADADOKFGFCPMAAHEICTTNEGVMYRIGDQMD 180

QY 197 KQHDMGHMRCTCVGNGRGEMTCA 221
DB 181 KQHDMGHMRCTCVGNGRGEMTCA 205

RESULT 5
O95610 PRELIMINARY; PRT; 379 AA.
AC O95610;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Fibronection (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Godfrey H.P., Ebrahim A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42404; AAD00015.1; -.
DR HSSP; P02751; 1FBR.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 6.
DR Pfam; PF00040; fn2; 2.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 5.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 4.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
FT NON_TER 1 379
FT NON_TER 379 379
SQ SEQUENCE 379 AA; 42191 MW; 319FF9C844059542 CRC64;

Query Match 54.5%; Score 1091; DB 4; Length 379;
Best Local Similarity 99.0%; Pred. No. 6.9e-95;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAYQOPHPQPPYGHCVTDSGVVSYVGMQLKTQGNKQMLCTCLGNGVSCQETAVTQ 61
DB 189 AAYQOPHPQPPYGHCVTDSGVVSYVGMQLKTQGNKQMLCTCLGNGVSCQETAVTQ 248

QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKYSFCTDHTVLVQ 121
DB 249 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKYSFCTDHTVLVQ 308

QY 122 RGSNSGALCHPPELYNNHNTYDCTSEGRDMMKMGCTTQNYADADOKFGFCPMAAHEIC 181
DB 309 RGSNSGALCHPPELYNNHNTYDCTSEGRDMMKMGCTTQNYADADOKFGFCPMAAHEIC 368

QY 182 TTNEGVMYRIG 192
DB 369 TTNEGVMYRIG 379

RESULT 6
O90X02 PRELIMINARY; PRT; 141 AA.
AC O90X02;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Fibronection (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC Ambystoma.
NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21439472; PubMed=11555861;
RA Christensen R.N., Weinstein M., Taasava R.A.;
RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT and semi-quantitative RT-PCR expression studies.";
RL J. Exp. Zool. 290:529-540 (2001).
DR EMBL; AF360987; AAL16960.1; -.
DR InterPro; IPR000083; Fibrnctnl.
DR Pfam; PF00039; fn1; 3.
DR PRINTS; PR00012; FNTYPEII.
DR SMART; SM00058; FN1; 3.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
FT NON_TER 1 141
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 16571 MW; F5E7443B27D2593C CRC64;

Query Match 37.5%; Score 750; DB 13; Length 141;
```

Best Local Similarity 87.9%; Pred. No. 3.7e-63;
Matches 124; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 169 FGFCPMAAHEICTTNEGVMRIGDQMDKHMGHMRCTCVGNGRGEMTCIAVSQALDQ 228
Db 1 FGFCPMAAHEICTTNEGVMRIGDQMDKHMGHMRCTCVGNGRGEMTCIAVSQALDQ 60

QY 229 CIVDDITYNVNDTFHKRHEEGHMLNCTCFGGGRMKCDPVDCQDSEGTFTFYIGDSWE 288
Db 61 CIVDDITYNVNDTFHKRHEEGHMLNCTCFGGGRMKCDPIDCQDSEGTFTFYIGDSWE 120

QY 289 KYVHGVRVQCYCGRGIGEMH 309
Db 121 KYVHGVRVQCYCGRGIGEMH 141

RESULT 7

Q98856 PRELIMINARY; PRT; 679 AA.
AC Q98856;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
OX NCBI_TaxId=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating new limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
DR EMBL; D82052; BA01523.1; -.
DR HSSP; P02751; 2FN2.
DR MEROPS; M10.004; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemoxelin.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; Zn_MTPeptidase.
DR InterPro; IPR06025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; hemoxelin; 4.
DR Pfam; PF00413; peptidase_M10_N; 1.
DR Pfam; PF03933; peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00013; MATRXIN.
DR ProDom; PD000955; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; znm; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOXELIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 679 AA; 75581 MW; 573CDB9DBF85524 CRC64;

Query Match 20.2%; Score 405; DB 13; Length 679;
Best Local Similarity 30.2%; Pred. No. 1e-29;
Matches 98; Conservative 39; Mismatches 88; Indels 100; Gaps 12;

QY 47 LGNVSOCEATVVTQYGGNSNGEPCVLPFTYNGRTFYSCCTEGQDGLMSTSTSNVED 106
Db 213 LGTV-----VVKTRFGNANGAACKFPFKNGNSYSTSEGRDGLMSTTTDDXD 266

QY 107 QKYSFCTDHTVLVOTRGNSNGALCHFPFLYNNHNYTCTSEGRDNMKMGCTTQNYDAD 166
Db 267 KKYVFCFCE--LTYTGNSDGDCKVFFPIFDGSDYDCTEGSDGGRWKATIDNPKD 324

QY 167 QKGFCEPMAAHEICTTNEGVMRIGDQMDKHMGHMRCTCV--GNGRGEMTCIAVSQ 224

Db 325 KKYVFCP-----NDTAVTGNSSQ----- 344
QY 225 LRDCIYDDITYNVNDTFHKRHEEGHMLNCTCFGGGRMKCDPVDCQDSEGTFTFYIGDSWE 275
Db 345 --DPCVPPPP--LEKTYH-----SCTSDGRGRKIMCATTSSYSDRKKGFPPDQ 391

QY 276 ETGTF---YQIGDS-----WEKYHGVRYO-----CYCGRGIGEMH 309
Db 392 GYSLFLVGAHFGHAIQLHSTYDALMPMFYIEGFOIHODDIEGVQYLYSGTGPHR 451

QY 310 CQPLQT--YPSSSQVGFITETPS 332
Db 452 SPPMPTKSPDVSGKTTTVTTSPT 476

RESULT 8

Q98F06 PRELIMINARY; PRT; 675 AA.
AC Q98F06;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Matrix metalloproteinase 9 precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C.M., Sangrador-Vegas A., Smith T.J.;
RT "Cloning and characterisation of the rainbow trout (Oncorhynchus
RT mykiss) mmp9 mRNA.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ320533; CAC85923.1; -.
DR HSSP; P39900; 1U1Z.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemoxelin.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; Zn_MTPeptidase.
DR InterPro; IPR06025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; hemoxelin; 4.
DR Pfam; PF00413; peptidase_M10_N; 1.
DR Pfam; PF03933; peptidase_M10_N; 1.
DR ProDom; PD000955; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; znm; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR HydroLase; Metal-binding; Metalloprotease; Protease; Signal; Zinc.
FT SIGNAL 1 19
SQ SEQUENCE 675 AA; 75261 MW; 84A78BD96BDB569E CRC64;

Query Match 19.6%; Score 392; DB 13; Length 675;
Best Local Similarity 27.8%; Pred. No. 1.7e-28;
Matches 105; Conservative 37; Mismatches 100; Indels 136; Gaps 14;

QY 10 HPOPPPG-----HCVTDSGVVSVGMQLKTQGNKO-MTC-----TCLNGV 51
Db 191 HAPFGGCIQGDHAFDDENWTLGKAAVYTSFGNAGALCHFPFSGGQYSTCTTEGR 250

QY 52 S-----QCEFA-----VTQYGGNSNGEPCVLPFTYNGRTFYSCCTEGROD 92
Db 251 SDNLPMCATTAADGRDKKFCSEBLLYTFDGNNGKACVFPFVLGETYEGCTTEGRSD 310

QY 93 GHLMGSTTSNVEDQKSFCTDHTVLVOTRGNSNGALCHFPFLYNNHNYTCTSEGRDN 152
Db 311 GYRWCSTTENFDKDKKGFQCPNBDTAV--TGNSEGBCHFPFVLGNKYDSCTSEGRD 368

[illegible]

ID	Q9PWS	PRELIMINARY	PRT	690 AA.
AC	Q9PWS			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2003	(TREMBLrel. 23, Last annotation update)		
DE	Gelatinase B.			
GN	GEL-B.			
OS	Oryzias latipes (Medaka fish) (Japanese ricefish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neuteleostei;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;			
OC	Acantiformes; Acanthichthyidae; Oryziinae; Oryzias.			
OX	NCBI_TaxID=8090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20363695; PubMed=10903498;			
RA	Matsui H., Ogiwara K., Ohkura R., Yamashita M., Takahashi T.;			
RT	"Expression of gelatinases A and B in the ovary of the medaka fish			
RT	Oryzias latipes.";			
RL	Eur. J. Biochem. 267:4658-4668(2000).			
DR	EMBL; AB033755; BAA85770.1; -.			
DR	HSSP; P08254; IHFS.			
DR	MEROFS; M10.004; -.			
DR	InterPro; IPR000562; FN_Type_II.			
DR	InterPro; IPR000585; Hemopexin.			
DR	InterPro; IPR001818; Matrixin.			
DR	InterPro; IPR006026; Nzn_MTPeptide.			
DR	InterPro; IPR006025; Zn_MTPeptide.			
DR	Pfam; PF00040; fn2; 3.			
DR	Pfam; PF00045; hemopexin; 4.			
DR	Pfam; PF00413; Peptidase M10; 1.			
DR	Pfam; PF03933; Peptidase M10_N; 1.			
DR	PRINTS; PR00013; ENTPeptI.			
DR	PRINTS; PR00138; MATRIXIN.			
DR	ProDom; PD000995; FN_Type_II; 3.			
DR	SMART; SMO0059; FN2; 3.			
DR	SMART; SMO0120; HX; 4.			
DR	SMART; SMO0235; ZmC; 1.			
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.			
DR	PROSITE; PS00023; FIBRONECTIN_2; 3.			
DR	PROSITE; PS00024; HEMOPEXIN; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
KW	Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.			
SEQUENCE	690 AA; 77610 MW; 43507186ED9BD088 CRC64;			
Q9PWS				
Query Match	19.5%;	Score 391;	DB 13;	Length 690;
Best Local Similarity	32.1%;	Pred. No. 2,1e-28;		
Matches	96;	Conservative 41;	Mismatches 116;	Indels 46;
				Gaps 10;
47	LGNGVSCCEIATVQYVGNSSNPECVLPFTYNGRTFYSCTEGRDGHMGCTSTNSYED	106		
214	LGKG-----DVVKYYGNADAMCHFPVFGKRYTCTSTSGRADKLLPWCSTTDYRD	267		

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QY      10  QKSFCTDHTVIVQRRGSGNGLCHPEFLVNNHNYDCTSEGRDMMKCGTTONDAD 166
Db      268  GKXGFCPSB--LTYITGGNSDAKCVFFVFLGSEYDSCTTEGRDRDYRCAITTSNDQD 325
QY      167  QKFGCPMAAHEICTTNEGVMYR-----IDQMDKDHGMKCTCVANGGE-W-T 218
Db      326  KKKGFCPNDTTTIGNAEGECPHPPEFLKEYDS-----CTSEGRGDKLMCGT 376
QY      219  CIAYSGLRQCCVDDITVANDTFHKHREBHMNLCTCFQGRGRMKCDPVDCQDSEFG 278
Db      377  TASVYDDDKMGFCPOQGYSL-FLVAALHFEHGLGL-----DHSNIRDLMY 421
QY      279  TFIQIGDSN--EKYVHGVRVQCYCYGRGIGEMHCOPLOTYSSSGEVAEITETPSOP 334
Db      422  PKSYVEDSLSHEDDIEGIQ--YLYGSKTPKPFVQPKPFTTATPDPDVDSIDEP 477

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RESULT	ID	PRELIMINARY	PRI	671 AA
09W7L6	09W7L6			
AC	01-NOV-1999	(TREMBlrel. 12, Created)		
DT	01-NOV-1999	(TREMBlrel. 12, Last sequence update)		
DT	01-MAR-2003	(TREMBlrel. 23, Last annotation update)		
DE	Gelatinase B.			
GN	MMP-9.			
OS	Xenopus laevis (African Clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Carinato M.E., Walter B.E., Henry J.J.;			
RT	"XMP-9 (Gelatinase B) is Expressed During Wound Healing,			
RT	Regeneration.";			
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF072455; AAD41624.1; -			
DR	HSSP; P08254; IUSN.			
DR	MEROPS; M10.004; -.			
DR	InterPro; IPR000562; FN_Type_II.			
DR	InterPro; IPR000585; Hemopexin.			
DR	InterPro; IPR001818; Matrxin.			
DR	InterPro; IPR006026; Nzn_MTPeptase.			
DR	InterPro; IPR006025; zn_MTPeptase.			
DR	Pfam; PF00040; fn2_3.			
DR	Pfam; PF00045; hemopexin_4.			
DR	Pfam; PF00413; peptidase_M10_1.			
DR	Pfam; PF03933; peptidase_M10_N_1.			
DR	PRINTS; PR00013; FNTYPEII.			
DR	PRINTS; PR00138; MATRXIN.			
DR	ProDom; PD000995; FN_Type_II; 3.			
DR	SMART; SMO0059; FN2_3.			
DR	SMART; SMO0130; HX; 4.			
DR	SMART; SMO0235; ZmC; 1.			
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.			
DR	PROSITE; PS00023; FIBRONECTIN_2; 3.			
DR	PROSITE; PS00024; HEMOPEXIN; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
KW	Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.			
SEQ	SEQUENCE 671 AA; 74845 MW; 1464052069FAFE CRC64;			
Query Match	19.5%; Score 389.5; DB 13; Length 671;			
Best Local Similarity	45.1%; Pred. No. 2.9e-28;			
Matches	74; Conservative 20; Mismatches 45; Indels 25; Gaps 4;			
QY	SVNQMIKLT-----QGNKQMLCTGLGNGVSGQETAVITQYGSNGGECVLPFTYNGRTF 82			
Db	SDGLPWCSTTNNYQDKKYGFC-----PEMLTYTGSGNSGCVLPFTFDGVSX 298			
QY	83 YSCITTEGRQDGLMCSTTSNYEQDKYSFCTDHTVLVOTRGNSNGALCHPPLLYNNHNY 142			
Db	299 NGCTKEGDDPYRNCSTTANFDQKYGFCENRDTSV--IGNSGGECEVPPFTLGRKH 356			

Db 419 MYPMYTVEDFSLHXKDIDEGIQLYGKGTG-----PDPPTPPPTSTTTTPN-PTG 467
 QY 337 HP 338
 Db 468 EP 469

RESULT 13
 ID 09N1P6 PRELIMINARY; PRT; 632 AA.
 AC 09N1P6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE Matrix metalloproteinase-2 (Fragment).
 OS MMP-2.
 GN Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISUE= fibrosarcoma;
 RA Jalic H., Paria B., Balkin R., Baxendale V., Fang Y., Kitchell B.;
 RT "Cloning of matrix metalloproteinase-2 (MMP-2) from canine
 fibrosarcoma.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF17217; AAF67517.1;
 DR HSSP; P08253; 1RTG.
 DR MEROPS; M10_003;
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; ENTPEPIL.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 FT NON_TER
 SQ SEQUENCE 632 AA; 70991 MW; D8AE895497E129F3 CRC64;

Query Match 19.1%; Score 381.5; DB 6; Length 632;
 Best Local Similarity 39.3%; Pred. No. 1.5e-27;
 Matches 81; Conservative 26; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTGGNSGECVLPFTYNGRTFVSCCTEGRQDGLMCSITSNYEDOKYSPCTD 114
 Db 189 EGVVAVKVGNAAGEYKPFPLNGREYVSTCTDGRSDGLMCSITNYFEXDKYGC-P 247
 QY 115 HTVLVOTRGNSGALCHPFLYNNHNYTDTCTSEGRDNMKKCGTTONTYADOKFGFCPM 174
 Db 248 HEALF-TMGGNADGOQPKPFPRFGTGSYSDCTTEGRTDGYRWCGTTEVDYDRDKYGFCEP 306
 QY 175 AAHEICTTNEG----MYRIGDQMDKQDMGMKRCCTCVGNGRGEMTQIA---YSQR 226
 Db 307 TASTTGNSGSEGAPCVFPFTFLGKES-----CTASGNSDGVKWCATTANYDDDR 357
 QY 227 DQCIIVDITYNVDTFKRHEEGHML 252
 Db 358 KMGFCPDQGYSL--FLVAHAHFGHAM 381

RESULT 14
 ID 09DE15 PRELIMINARY; PRT; 686 AA.
 AC 09DE15;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE 75 kDa gelatinase.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20576236; PubMed=11010969;
 RA Hahn-Dantona E.A., Ames R.T., Quigley J.P.;
 RT "The isolation, characterization, and molecular cloning of a 75-kDa
 gelatinase B-like enzyme, a member of the matrix metalloproteinase
 (MMP) family. An avian enzyme that is MMP-9-like in its cell
 expression pattern but diverges from mammalian gelatinase B in
 sequence and biochemical properties.";
 RL J. Biol. Chem. 275:40827-40838(2000).
 DR EMBL; AF222690; AAG47650.1;
 DR HSSP; P08254; ISLM.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; ENTPEPIL.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 686 AA; 76679 MW; 9E9AB59F6A497CE CRC64;

Query Match 19.0%; Score 379.5; DB 13; Length 686;
 Best Local Similarity 28.7%; Pred. No. 2.6e-27;
 Matches 99; Conservative 45; Mismatches 82; Indels 119; Gaps 15;

QY 16 YGHCVTDGVSIVGQMLTKQGNKQMLCT---CLGNQVSCQETAVTQYGGNSGECV 72
 Db 241 YSKCITEG--RDGGLMKATTASVADKTYGC-----PSLLYTNNGNSDGSPCV 289
 QY 73 LPFTYNGRTFVSCCTEGRQDGLMCSITSNYEDOKYSPCTD-tylvotrgnsngalc 131
 Db 290 FPFIFDGASVDTCTDGRSDGYRWCGTTFANFDQDKYGCPRNDTAAI---GNSQDDPC 346
 QY 132 HPFLYNNHNYTDTCTSEGRDNMKKCGTTONTYADOKFGFCP-----MAHEICTT 183
 Db 347 VFPTFLGYSYRSITQGRQDGLMCAITTSNVDTKRWGCPDRGYSIFLVAHE----- 401
 QY 184 NEGMYRIGDQMDKQDMGMKRCCTCVGNGRGEMTQIAVSQLRDQCIIVDITYNVDTFH 243
 Db 402 -----FGHSIG-----LDHSSVTEALMYPYIS-YVD--F 428
 QY 244 KRHEEGHMLNCTCGGGRGRWKCDDVDCODESETGTFTYQISWEKRYHGVRYQCYGR 303
 Db 429 QLHEDD-----VGGIQ---YLYGR 444

QY 304 GIGEMHCOPL-----QTPSSSG--PVEVFTETPSQPNHP 338
 DB 445 GSGEPPTPPAPLPTEEPQSIPTKEAGSASTEEBEETP-EPTAPB 488

RESULT 15

Q95J4 PRELIMINARY; PRT; 661 AA.
 AC Q95J4;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Gelatinase A.
 GN MMP-2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Enamel organ;
 RA Caron C., Xue J., Bartlett J.D.;
 RT "Localization of Gelatinase A (MMP-2) in developing tooth tissues and
 RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RU EMBL; AF295805; AAK97133.1; -
 DR HSSP; P39900; 1U1Z.
 DR MEROPS; M10.003; -
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzh_MTpeptidase.
 DR InterPro; IPR006025; Zn_MTpeptidase.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; peptidase_M10; 1.
 DR Pfam; PF03933; peptidase_M10_N; 1.
 DR PRINTS; PRO00138; FNTYPEII.
 DR PRINTS; PRO0013; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZNMG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 661 AA; 73669 MW; 41CD448BD72DCC2 CRC64;

Query Match 18.9%; Score 378.5; DB 6; Length 661;
 Best Local Similarity 37.9%; Pred. No. 3, 1e-27;
 Matches 78; Conservative 30; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVTQYGGNSNGEPCVLPPTVNGRTFYCTTBGRDGLHMCSTTSNYEDOKYSFCTD 114
 DB 218 EGQVRYVYGVNADGEYCKFPSPFNGKEXYNSCTDGRSDGFLWCSTYVFDKGYGFC-P 276
 QY 115 HTVAVQIRGNSNGALCHPEFLYNNHNTDCTSGRBDNMKCGTQNYADOKRGPCPM 174
 DB 277 HEALP-TWGNADQPCPKFPFQGTSTNSCTTBGRDGYRWCGTTEYDRDKKYGFCPE 335
 QY 175 AAHEICTTNEG------MYRIGDQMDKQDMGHMRCTGVNGRGEWTGIA--YSQLR 226
 DB 336 TAWSTVGNSRGAQCVFPFTFLGNKHS-----CTSAGRSDGKLMCAITANYDDDR 386
 QY 227 DQCIVDITVAVNDTFKRRHEGHML 252
 DB 387 KWGFCPDQGYSL--FLVAHHEFGHAM 410

Search completed: November 28, 2003, 15:01:35
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 21 Seconds

(Without alignments)
1570.755 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002

Sequence: 1 MAAVYQPPHPQPPYGHCV.....EVFTTPSQPNHPQWLE 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	98.9	2386	1 FNMU	fibronectin precu
2	1927	96.3	2265	1 FNBO	fibronectin - bovi
3	1877	93.8	2477	2 S14428	fibronectin precu
4	1601	80.0	2481	2 A43908	fibronectin - Afri
5	961	48.0	190	2 I51279	fibronectin - east
6	396.5	19.8	707	1 A53786	gelatinase B (EC 3
7	393	19.6	708	2 UC4364	gelatinase B (EC 3
8	386.5	19.3	662	2 S70365	gelatinase A (EC 3
9	385.5	19.3	662	2 A42496	gelatinase A (EC 3
10	385.5	19.3	662	2 S34780	gelatinase A (EC 3
11	382.5	19.1	660	1 A28153	gelatinase A (EC 3
12	382.5	19.1	663	1 S46492	gelatinase A (EC 3
13	382	19.1	708	2 S62907	gelatinase B (EC 3
14	382	19.1	730	1 I52580	gelatinase B (EC 3
15	382	19.1	730	1 I52580	gelatinase B (EC 3
16	381	19.0	712	1 A46031	gelatinase B (EC 3
17	374	18.7	707	1 A34458	gelatinase B (EC 3
18	203	10.1	1326	2 B56385	secretory phosphol
19	203	10.1	1465	2 A56385	secretory phosphol
20	202	10.1	1455	2 A48925	mannose receptor p
21	195.5	9.6	1463	2 A53210	phospholipase A2 r
22	193	9.6	1456	2 A36563	mannose receptor p
23	189.5	9.5	1458	2 A49707	phospholipase A2 r
24	187	9.3	1479	2 T42710	mannose receptor,
25	181	9.0	121	2 S58424	seminal plasma pro
26	180.5	9.0	1487	2 S48719	phospholipase-A(2)
27	175.5	8.8	105	2 A58837	DH sperm surface
28	170	8.5	655	1 A46688	hepatocyte growth
29	166.5	8.3	115	2 A29156	seminal fluid prot

30	165	8.2	615	1 KFHU12	coagulation factor
31	164.5	7.9	2482	2 WTBO	seminal fluid prot
32	159	7.9	2482	2 I48922	cation-independent
33	159	7.9	2483	1 A49617	insulin-like growt
34	156.5	7.8	2491	1 A28372	insulin-like growt
35	156.5	7.8	2499	1 A30788	mannose 6-phosphat
36	154	7.7	593	2 S45281	coagulation factor
37	151.5	7.6	2470	2 I50726	cation-independent
38	148.5	7.4	1020	2 A29355	fibronectin - chic
39	144	7.2	603	2 S28841	coagulation factor
40	140.5	7.0	1723	2 S58880	receptor DBC-205 -
41	134.5	6.7	719	2 T00266	hypothetical prote
42	125	6.2	922	2 T23573	hypothetical prote
43	125	6.2	3712	2 I18253	laminin alpha-1 ch
44	122	6.1	551	2 I46709	endothelial leukoc
45	120	6.0	23	2 B43836	fibronectin - rabb

ALIGNMENTS

RESULT 1

FNMU
fibronectin precursor [validated] - human
N:Alternate names: fibronectin splice form ED-A
C:Species: Homo sapiens (man)
C>Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 08-Dec-2000
C/Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A221
R/Dean, D.C.; Bowlin, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A>Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; PMID:8715578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A/Cross-references: GB:M15801; NID:G182686; PIDN:AA53376.1; PID:G553293
R/Poole, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A>Title: Evolution of the fibronectin gene.
A:Reference number: A26284; PMID:86111901; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A/Cross-references: GB:M12549; NID:G182688
A>Note: the authors translated the codon TTC for residue 1494 as Glu
R/Poole, A.; Hendrich, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A>Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A:Reference number: S00848; PMID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA
A:Residues: 1594-1767, 'V', 1769-1783 <PAO>
A/Cross-references: EMBL:X07718; NID:G31402
A>Note: the authors translated the codon AAC for residue 1631 as Asp
R/Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A>Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
A:Reference number: A24854; PMID:87030929; PMID:3770201
A:Accession: A24854
A:Molecule type: DNA
A:Residues: 1992-2147 <VIB>
A/Cross-references: GB:X04530; NID:G31436
R/Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A>Title: Human fibronectin is synthesized as a pre-propolypeptide.
A:Reference number: A24476; PMID:87030890; PMID:3770189
A:Accession: A24476
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, 'Q', 16-38 <GUT>
R/Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A>Title: Primary structure of human fibronectin: differential splicing may generate at le

A/Reference number: A91008; MUID:85284965; PMID:2992939
A/Accession: A91008
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
A/Cross-references: GB:X02761
R/Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5866, 1984
A/Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A/Reference number: A93529; MUID:84272258; PMID:6462919
A/Accession: A93529
A/Molecule type: mRNA
A/Residues: 975-2080, 2112-2386 <KOR>
A/Cross-references: GB:X00739
R/Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A/Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A/Reference number: A21011; MUID:83290929; PMID:6688418
A/Accession: A21011
A/Molecule type: mRNA
A/Residues: 1434-1537 <OL2>
A/Cross-references: GB:K00055; NID:G182680; PIDN:AAA52459.1; PID:G182683
R/Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A/Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A/Reference number: A90495; MUID:85280409; PMID:2992573
A/Accession: A90495
A/Molecule type: mRNA
A/Residues: 1594-2386 <BRR>
A/Cross-references: GB:M10905; NID:G182696; PIDN:AAA52462.1; PID:G182697
R/Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A/Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A/Reference number: A22245; MUID:85231203; PMID:2989004
A/Accession: A22245
A/Molecule type: mRNA
A/Residues: 1948-2067 <UME>
A/Cross-references: GB:M27589; NID:G182705; PIDN:AAA52465.1; PID:G182706
A/Accession: B22245
A/Molecule type: mRNA
A/Residues: 1975-1991, 2017-2039 <UM2>
A/Cross-references: GB:M27590
R/Sekiuchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A/Title: Human liver fibronectin complementary DNAs: identification of two different mes
A/Reference number: 152394; MUID:87026578; PMID:3021206
A/Accession: 152373
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
A/Cross-references: GB:M14060; NID:G182701; PIDN:AAA52464.1; PID:G182704
R/Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A/Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A/Reference number: A21165; MUID:83221567; PMID:6304699
A/Accession: A21165
A/Molecule type: mRNA
A/Residues: 2291-2386 <KOR>
A/Cross-references: GB:K00799; NID:G182681; PIDN:AAA52460.1; PID:G182684
R/Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A/Title: Primary structure of human plasma fibronectin.
A/Reference number: A92398; MUID:84032463; PMID:6630202
A/Accession: A92398
A/Molecule type: protein
A/Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R/Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A/Title: Further characterization of the binding of fibronectin to gelatin reveals the p
A/Reference number: S34791; MUID:93312001; PMID:832285
A/Accession: S34791
A/Molecule type: protein
A/Residues: 291-300, 551-560 <GAR2>

R/Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A/Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A/Reference number: A60904; MUID:87019725; PMID:3552418
A/Accession: A60904
A/Molecule type: protein
A/Residues: 293-301 <GR1>
R/Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Sirt, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A/Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human p
A/Reference number: A23901; MUID:6608277; PMID:3900070
A/Accession: A23901
A/Molecule type: protein
A/Residues: 616-677, 'Q', 679-703, 'PR' <CAL>
R/Pierzbacher, M.D.; Ruoslahti, E.; Sundell, J.; Land, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A/Title: The cell attachment domain of fibronectin. Determination of the primary structu
A/Reference number: A92386; MUID:82265604; PMID:7050098
A/Accession: A92386
A/Molecule type: protein
A/Residues: 1441-1548 <PIE>
A/Note: residues 1524-1527 are responsible for the cell-binding activity
R/Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A/Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dome
A/Reference number: A32517; MUID:87241275; PMID:3593220
A/Accession: A32517
A/Molecule type: protein
A/Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R/Ritschel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pande
Biochem. J. 274, 731-738, 1991
A/Title: Human plasma fibronectin. Demonstration of structural differences between the A-
A/Reference number: S14357; MUID:91190085; PMID:2012601
A/Accession: S14357
A/Molecule type: protein
A/Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRB>
R/Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A/Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalt
A/Reference number: A23891; MUID:85261459; PMID:4019516
A/Accession: A23891
A/Molecule type: protein
A/Residues: 2071-2080, 2112-2356 <GAR4>
C/Comment: The extra domain and connecting strand 3 are subject to developmental and tise
C/Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
ation, and transformation.
C/Genetics:
A/Gene: GDB:FNI
A/Cross-references: GDB:119135; OMIM:135600
A/Map position: 2q34-2q34
A/Intons: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C/Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicati
F/1-6/Domain: signal sequence #status predicted <SIG>
F/27-31/Domain: propeptide #status predicted <PRO>
F/32-2386/Product: fibronectin #status experimental <AMT>
F/52-87/Domain: fibrin and heparin binding <FHB>
F/52-272/Domain: fibrin and heparin binding <FHB>
F/97-135/Domain: fibronectin type I repeat homology <1F1>
F/141-179/Domain: fibronectin type I repeat homology <1F2>
F/186-225/Domain: fibronectin type I repeat homology <1F3>
F/231-270/Domain: fibronectin type I repeat homology <1F4>
F/308-608/Domain: collagen binding <CBR>
F/308-342/Domain: fibronectin type I repeat homology <1F5>
F/360-401/Domain: fibronectin type II repeat homology <1F6>
F/420-461/Domain: fibronectin type II repeat homology <2F1>
F/470-508/Domain: fibronectin type I repeat homology <1F7>
F/518-555/Domain: fibronectin type I repeat homology <1F8>
F/561-599/Domain: fibronectin type I repeat homology <1F9>
F/609-692/Domain: fibronectin type III repeat homology <3FA>
F/616-706/Domain: heparin binding <HRB>
F/719-801/Domain: fibronectin type III repeat homology <3FB>
F/810-891/Domain: fibronectin type III repeat homology <3FC>

F:906-988/Domain: fibronectin type III repeat homology <3FD>
 F:996-1077/Domain: fibronectin type III repeat homology <3FE>
 F:1086-1164/Domain: fibronectin type III repeat homology <3FF>
 F:1173-1258/Domain: fibronectin type III repeat homology <3FG>
 F:1266-1349/Domain: fibronectin type III repeat homology <3FH>

Query Match 98.4%; Score 1979; DB 1; Length 2386;
 Best Local Similarity 99.4%; Pred. No. 1,9e-140;
 Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAYVQPHQPPYGHCTVDSGVVSVGMQMLKTGQNKQMLCTCLGNGVSCQETAVTQT 61
 DB 291 AAYVQPHQPPYGHCTVDSGVVSVGMQMLKTGQNKQMLCTCLGNGVSCQETAVTQT 350
 QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSNVBDQKXSCDHTLVQTR 121
 DB 351 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSNVBDQKXSCDHTLVQTR 410
 QY 122 RGSNSGALCHFPFLYNNHYTDTCTSEGRDNMKMCTTQNYDADQKFGCPMAAHEICT 181
 DB 411 QGNSNGALCHFPFLYNNHYTDTCTSEGRDNMKMCTTQNYDADQKFGCPMAAHEICT 470
 QY 182 TTNEGVMYRIGDQMDKHDMGHMRCCTCVNGRGEMTCLAYSQLRDQCIYDITVYVNDT 241
 DB 471 TTNEGVMYRIGDQMDKHDMGHMRCCTCVNGRGEMTCLAYSQLRDQCIYDITVYVNDT 530
 QY 242 FHKRHEGHMLNCTCGQGRGRMKCDPVQCCDSEFTFYQIGDSWEKYNHGVRYQCYC 301
 DB 531 FHKRHEGHMLNCTCGQGRGRMKCDPVQCCDSEFTFYQIGDSWEKYNHGVRYQCYC 590
 QY 302 GRGIGEMHCOPLQTYPTSSSGPVEVFTETPSQNSHPICW 341
 DB 591 GRGIGEMHCOPLQTYPTSSSGPVEVFTETPSQNSHPICW 630

RESULT 2

FNBO
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1988 #sequence, revision 31-Dec-1988 #ext, change 20-Oct-2000
 C:Accession: A26452; B21165; A23292
 R:Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
 Eur. J. Biochem. 161, 441-453, 1986
 A:Title: Complete primary structure of bovine plasma fibronectin.
 A:Reference number: A26452; MVID:87054047; PMID:3780752
 A:Accession: A26452
 A:Molecule type: protein
 A:Residues: 1-2265 <SKO>
 R:Korblint, A.R.; Vide-Pedersen, K.; Baralle, F.E.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
 A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
 A:Reference number: A21165; MVID:83221567; PMID:6504699
 A:Accession: B21165
 A:Molecule type: mRNA
 A:Residues: 2170-2265 <KOR>
 A:Cross-references: GB:K00800; NID:g163055; PIND:AAA30521.2; PID:g5713323
 R:Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vide-Pedersen, K.; Sahl, P.; Sott
 Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
 A:Title: Partial primary structure of bovine plasma fibronectin: three types of internal
 A:Reference number: A23292; MVID:83117805; PMID:6218503
 A:Accession: A23292
 A:Molecule type: protein
 A:Residues: 116, 'C', 18-20, 'S', 22-43, 447-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-226
 C:Comment: Cys-1201 and Cys-2015 have free sulphydryl groups.
 C:Comment: The plasma fibronectin molecule consists of two chains, which are connected b
 aing, and maintenance of cell shape.
 C:Comment: Plasma fibronectin is synthesized by hepatocytes.
 C:superfamily: fibronectin fibronectin type I repeat homology; fibronectin type II repe
 C:Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellu
 F:21-241/Domain: fibrin binding <FBR>
 F:21-56/Domain: fibronectin type I repeat homology <1F1>
 F:66-104/Domain: fibronectin type I repeat homology <1F2>

F:110-148/Domain: fibronectin type I repeat homology <1F3>
 F:155-194/Domain: fibronectin type I repeat homology <1F4>
 F:200-239/Domain: fibronectin type I repeat homology <1F5>
 F:277-577/Domain: collagen binding <CBR>
 F:277-511/Domain: fibronectin type I repeat homology <1F6>
 F:329-370/Domain: fibronectin type II repeat homology <2F1>
 F:389-430/Domain: fibronectin type II repeat homology <2F2>
 F:439-477/Domain: fibronectin type I repeat homology <1F7>
 F:487-524/Domain: fibronectin type I repeat homology <1F8>
 F:530-568/Domain: fibronectin type I repeat homology <1F9>
 F:578-661/Domain: fibronectin type III repeat homology <FN3A>
 F:688-770/Domain: fibronectin type III repeat homology <FN3B>
 F:779-860/Domain: fibronectin type III repeat homology <FN3C>
 F:875-957/Domain: fibronectin type III repeat homology <FN3D>
 F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
 F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
 F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
 F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>
 F:1326-1404/Domain: fibronectin type III repeat homology <GN3I>
 F:1410-1517/Domain: cell attachment <CAD>
 F:1416-1502/Domain: fibronectin type III repeat homology <FN3J>
 F:1493-1495/Domain: cell attachment (R-G-D) motif
 F:1510-1592/Domain: fibronectin type III repeat homology <FN3K>
 F:1600-1870/Domain: heparin binding <HB2>
 F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>
 F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>
 F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>
 F:1970-1972/Domain: cell attachment (R-G-D) motif
 F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
 F:1985-2216/Domain: fibrin binding <FB2>
 F:2085-2124/Domain: fibronectin type I repeat homology <1F10>
 F:2130-2167/Domain: fibronectin type I repeat homology <1F11>
 F:2174-2209/Domain: fibronectin type I repeat homology <1F12>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
 F:21-47, 45-56, 66-94, 92-104, 110-138, 136-148, 155-184, 182-194, 200-229, 227-239, 277-304, 302-31
 7, 2155-2167, 2174-2200, 2198-2209/Dismulfide bonds: #status predicted
 F:399, 497, 511, 846, 976, 1213, 1987/Binding site: carboxylate (Asn) (covalent) #status exper
 F:1205, 1692/Binding site: carboxylate (Asn) (covalent) #status absent
 F:1943, 1944/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:2246/Dismulfide bonds: interchain (to 2250) #status predicted
 F:2250/Dismulfide bonds: interchain (to 2246) #status predicted
 F:2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 96.3%; Score 1927; DB 1; Length 2265;
 Best Local Similarity 96.5%; Pred. No. 1.5e-136;
 Matches 327; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 AAYVQPHQPPYGHCTVDSGVVSVGMQMLKTGQNKQMLCTCLGNGVSCQETAVTQT 62
 DB 261 AAYVQPHQPPYGHCTVDSGVVSVGMQMLKTGQNKQMLCTCLGNGVSCQETAVTQT 320
 QY 63 GGSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSNVBDQKXSCDHTLVQTR 122
 DB 321 GGSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSNVBDQKXSCDHTLVQTR 380
 QY 123 GGSNGALCHFPFLYNNHYTDTCTSEGRDNMKMCTTQNYDADQKFGCPMAAHEICT 182
 DB 381 GGSNGALCHFPFLYNNHYTDTCTSEGRDNMKMCTTQNYDADQKFGCPMAAHEICT 440
 QY 183 TTNEGVMYRIGDQMDKHDMGHMRCCTCVNGRGEMTCLAYSQLRDQCIYDITVYVNDT 242
 DB 441 TTNEGVMYRIGDQMDKHDMGHMRCCTCVNGRGEMTCLAYSQLRDQCIYDITVYVNDT 500
 QY 243 FHKRHEGHMLNCTCGQGRGRMKCDPVQCCDSEFTFYQIGDSWEKYNHGVRYQCYC 302
 DB 501 FHKRHEGHMLNCTCGQGRGRMKCDPVQCCDSEFTFYQIGDSWEKYNHGVRYQCYC 560
 QY 303 RIGIGEMHCOPLQTYPTSSSGPVEVFTETPSQNSHPICW 341
 DB 561 RIGIGEMHCOPLQTYPTSSSGPVEVFTETPSQNSHPICW 599

RESULT 3

fibronectin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text change 20-Aug-1999
C:Accession: S14428, S12455, A22319, S46203, S00459, A27252, I59049
R:Hynek, R.O.
submitted to the EMBL Data Library, July 1989
A:Reference number: S14428
A:Accession: S14428
A:Molecule type: mRNA
A:Residues: 1-2477 <R>
A:Cross-references: EMBL:X15906; NID:G56163; PIDN:CAA34020.1; PID:G56164
R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynek, R.O.
EMBO J. 6, 2573-2580, 1987
A:Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A:Reference number: S12455; MUID:88054951; PMID:12445560
A:Accession: S12455
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 609-1810, 'T', 1812-2283 <SCH>
A:Cross-references: EMBL:X15906
R:Tamkun, J.W.; Schwarzbauer, J.E.; Hynek, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A:Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing.
A:Reference number: A22319; MUID:84298097; PMID:6089177
A:Accession: A22319
A:Molecule type: DNA
A:Residues: 2052-2237 <TAM>
R:Faikheberg, C.; Engblid, U.J.; Thøgersen, I.B.; Salvesen, G.; Åkerstrøm, B.
Biochem. J. 301, 745-751, 1994
A:Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex intracellular mRNAs.
A:Reference number: S46203; MUID:94330948; PMID:7519849
A:Accession: S46203
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1183-1192, 'GAN', 1268, 'P', 1270-1271, 'D', 1273, 'GF', 1276, 'PY', 1385-1399 <PAL>
R:Patel, R.S.; Odematt, E.; Schwarzbauer, J.E.; Hynek, R.O.
EMBO J. 6, 2565-2572, 1987
A:Title: Organization of the rat fibronectin gene provides evidence for exon shuffling during evolution.
A:Reference number: S00459; MUID:88054950; PMID:3119323
A:Accession: S00459
A:Molecule type: DNA
A:Residues: 1-139; 2382-2477 <PAT>
A:Cross-references: EMBL:X05831
A:Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R:Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynek, R.O.
Cell 35, 421-431, 1983
A:Title: Three different fibronectin mRNAs arise by alternative splicing within the coding region of the rat fibronectin gene.
A:Reference number: A27252; MUID:84082067; PMID:6317187
A:Accession: A27252
A:Molecule type: mRNA
A:Residues: 1586-1720, 'T', 1722, 1813-2477 <SCS>
R:Odematt, E.; Tamkun, J.W.; Hynek, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A:Title: Repeating modular structure of the fibronectin gene: Relationship to protein structure.
A:Reference number: I59049; MUID:86016741; PMID:3863113
A:Accession: I59049
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1722-1810 <RES>
A:Cross-references: GB:M11750; NID:G204164; PIDN:AAA41170.1; PID:G554437
C:Genetics:
A:Insertions: 51/1; 94/1, 2416/3; 2454/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type III repeat homology; fibronectin type IV repeat homology; fibronectin type V repeat homology; fibronectin type VI repeat homology; fibronectin type VII repeat homology; fibronectin type VIII repeat homology; fibronectin type IX repeat homology; fibronectin type X repeat homology; fibronectin type XI repeat homology; fibronectin type XII repeat homology; fibronectin type XIII repeat homology; fibronectin type XIV repeat homology; fibronectin type XV repeat homology; fibronectin type XVI repeat homology; fibronectin type XVII repeat homology; fibronectin type XVIII repeat homology; fibronectin type XIX repeat homology; fibronectin type XX repeat homology; fibronectin type XXI repeat homology; fibronectin type XXII repeat homology; fibronectin type XXIII repeat homology; fibronectin type XXIV repeat homology; fibronectin type XXV repeat homology; fibronectin type XXVI repeat homology; 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fibronectin type XXXXXXXXXXVII repeat homology; fibronectin type XXXXXXXXXXVIII repeat homology; fibronectin type XXXXXXXXXXIX repeat homology; fibronectin type XXXXXXXXXXI repeat homology; fibronectin type XXXXXXXXXXII repeat homology; fibronectin type XXXXXXXXXXIII repeat homology; fibronectin type XXXXXXXXXXIV repeat homology; fibronectin type XXXXXXXXXXV repeat homology; fibronectin type XXXXXXXXXXVI repeat homology; fibronectin type XXXXXXXXXXVII repeat homology; fibronectin type XXXXXXXXXXVIII repeat homology; fibronectin type XXXXXXXXXXIX repeat homology; fibronectin type XXXXXXXXXXI repeat homology; fibronectin type XXXXXXXXXXII repeat homology; fibronectin type XXXXXXXXXXIII repeat homology; fibronectin type XXXXXXXXXXIV repeat homology; fibronectin type XXXXXXXXXXV repeat homology; fibronectin type XXXXXXXXXXVI repeat homology; fibronectin type XXXXXXXXXXVII repeat homology; fibronectin type XXXXXXXXXXVIII repeat homology; fibronectin type XXXXXXXXXXIX repeat homology; fibronectin type XXXXXXXXXXI repeat homology; 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fibronectin type XXXXXXXXXXI repeat homology; fibronectin type XXXXXXXXXXII repeat homology; fibronect

F.308-343/Domain:	fibronectin type I repeat homology <1F6>
F.360-401/Domain:	fibronectin type II repeat homology <2F1>
F.420-461/Domain:	fibronectin type II repeat homology <2F2>
F.470-508/Domain:	fibronectin type I repeat homology <1F7>
F.518-555/Domain:	fibronectin type I repeat homology <1F8>
F.561-599/Domain:	fibronectin type I repeat homology <1F9>
F.603-692/Domain:	fibronectin type III repeat homology <FN3A>
F.718-800/Domain:	fibronectin type III repeat homology <FN3B>
F.809-890/Domain:	fibronectin type III repeat homology <FN3C>
F.905-987/Domain:	fibronectin type III repeat homology <FN3D>
F.995-1076/Domain:	fibronectin type III repeat homology <FN3E>
F.1085-1164/Domain:	fibronectin type III repeat homology <FN3F>
F.1172-1257/Domain:	fibronectin type III repeat homology <FN3G>
F.1285-1348/Domain:	fibronectin type III repeat homology <FN3H>
F.1356-1439/Domain:	fibronectin type III repeat homology <FN3I>
F.1447-1529/Domain:	fibronectin type III repeat homology <FN3J>
F.1537-1619/Domain:	fibronectin type III repeat homology <FN3K>
F.1614-1616/Region:	cell attachment (R-G-D) motif
F.1631-1713/Domain:	fibronectin type III repeat homology <FN3L>
F.1721-1803/Domain:	fibronectin type III repeat homology <FN3M>
F.1811-1893/Domain:	fibronectin type III repeat homology <FN3N>
F.1903-1984/Domain:	fibronectin type III repeat homology <FN3O>
F.1992-2074/Domain:	fibronectin type III repeat homology <FN3P>
F.2181-2183/Region:	cell attachment (R-G-D) motif
F.2193-2273/Domain:	fibronectin type III repeat homology <FN3Q>
F.2296-2335/Domain:	fibronectin type I repeat homology <1F10>
F.2341-2378/Domain:	fibronectin type I repeat homology <1F11>
F.2385-2420/Domain:	fibronectin type I repeat homology <1F12>
F.53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 233-261, 259-271, 308-335, 333-368, 366-2378, 2385-2411, 2409-2420/Dsulfide bonds:	#status predicted
F.2458/Dsulfide bonds:	interchain (to 2462) #status predicted
F.2462/Dsulfide bonds:	interchain (to 2458) #status predicted

[illegible]

A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA

A/Residues: 1-2481 <DES>

A/Cross-references: GB:M77820

A/Note: sequence extracted from NCBI backbone (NCBI:P:77473)

C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

C/Keywords: duplication; extracellular matrix; glycoprotein; heterodimer

F/55-90/Domain: fibronectin type I repeat homology <1F1>

F/100-138/Domain: fibronectin type I repeat homology <1F2>

F/144-182/Domain: fibronectin type I repeat homology <1F3>

F/189-228/Domain: fibronectin type I repeat homology <1F4>

F/234-273/Domain: fibronectin type I repeat homology <1F5>

F/309-343/Domain: fibronectin type I repeat homology <1F6>

F/421-462/Domain: fibronectin type II repeat homology <2F1>

F/471-509/Domain: fibronectin type II repeat homology <2F2>

F/519-556/Domain: fibronectin type I repeat homology <1F7>

F/562-600/Domain: fibronectin type I repeat homology <1F8>

F/610-693/Domain: fibronectin type III repeat homology <FN3A>

F/719-801/Domain: fibronectin type III repeat homology <FN3B>

F/810-891/Domain: fibronectin type III repeat homology <FN3C>

F/906-988/Domain: fibronectin type III repeat homology <FN3D>

F/996-1077/Domain: fibronectin type III repeat homology <FN3E>

F/1086-1165/Domain: fibronectin type III repeat homology <FN3F>

F/1173-1258/Domain: fibronectin type III repeat homology <FN3G>

F/1266-1349/Domain: fibronectin type III repeat homology <FN3H>

F/1357-1440/Domain: fibronectin type III repeat homology <FN3I>

F/1448-1530/Domain: fibronectin type III repeat homology <FN3J>

F/1538-1620/Domain: fibronectin type III repeat homology <FN3U>

F/1615-1617/Region: cell attachment (R-G-D) motif

F/1632-1714/Domain: fibronectin type III repeat homology <FN3L>

F/1722-1804/Domain: fibronectin type III repeat homology <FN3M>

F/1812-1894/Domain: fibronectin type III repeat homology <FN3N>

F/1904-1985/Domain: fibronectin type III repeat homology <FN3O>

F/1993-2075/Domain: fibronectin type III repeat homology <FN3P>

F/2197-2277/Domain: fibronectin type III repeat homology <FN3Q>

F/2301-2340/Domain: fibronectin type I repeat homology <1F10>

F/2346-2383/Domain: fibronectin type I repeat homology <1F11>

F/2390-2425/Domain: fibronectin type I repeat homology <1F12>

F/255-81-79-90,100-128,126-138,144-172,170-182,189-218,216-228,234-263,261-273,309-336,33

F/2373,2371-2383,2390-2416,2414-2425/Disulfide bonds: #status predicted

F/2459/Disulfide bonds: interchain (to 2463) #status predicted

F/2463/Disulfide bonds: interchain (to 2459) #status predicted

Query Match 80.0%; Score 1601; DB 2; Length 2481;

Best Local Similarity 77.9%; Pred. No. 4.7e-112;

Matches 264; Conservative 41; Mismatches 32; Indels 2; Gaps 1;

3 AAYOROPHPRPYGHCVTSGVYVSGMOMLTKQGNKQMLCTCLGNGVSCOEPAATVQTY 62

295 ALYQPD--SOLBEPYGHCVTSGVYVSGMOMLTKQGNKQMLCTCLGNGVSCOEPAATVQTY 352

63 GGNNGEPVCLPFTYNGRTFYSCTTEGRQDGHLMCSFTTSYEDQKYSFCTDHTVAVQTR 122

353 GGNANGPACAPFTTHQKTYTSCSSEGRQDQKLMCATTSYDSDPKKYSFCTEDALAVQTR 412

123 GGNNGALCHPPLVYNNHNTDCTSEGRDNNMKCGTTQYVADQKFGCPMAAHEICT 182

413 GGNNGALCHPPLVYNNHNTDCTSEGRDNNMKCGTTQYVADQKFGCPMAAHEICT 472

183 TNGSVYWRIGSDQMDKQDMHMRCTGVNGRGWTCIAVSQALDQCTIVDITVYNNVDTF 242

473 TNGSVYWRIGSDQMDKQDMHMRCTGVNGRGWTCIAVSQALDQCTIVDITVYNNVDTF 532

243 HKHEBGMNLCTCFGGGRGKMKCDPVQDQDSEFTGTFTYQIGDSWEKTVHGVYQCYG 302

533 TKLHEBGMNLCTCFGGGRGKMKCDPVQDQDSEFTGTFTYQIGDSWEKTVHGVYQCYG 592

303 KGIQEWHCOPLOTPSSSGVYEVFTTTPSQPNSHPIQW 341

593 KGIQEWHCOPLOTPSSSGVYEVFTTTPSQPNSHPIQW 631

RESULT 5

151279

fibronectin - eastern newt (fragment)

C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999

C/Accession: 151279

R/Nace, J.D.; Tassava, R.A.

Dev. Dyn. 202; 153-164, 1995

A/Title: Examination of fibronectin distribution and its sources in the regenerating newt

A/Reference number: 151279; PMID:95252528; PMID:7734733

A/Accession: 151279

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-190 <NAC>

A/Cross-references: GB:S76886; NID:914305; PIRN:AA834250.1; PID:914306

C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

F/7-48/Domain: fibronectin type II repeat homology <2F2>

F/57-95/Domain: fibronectin type I repeat homology <1F7>

F/105-142/Domain: fibronectin type I repeat homology <1F8>

F/148-186/Domain: fibronectin type I repeat homology <1F9>

Query Match 48.0%; Score 961; DB 2; Length 190;

Best Local Similarity 85.8%; Pred. No. 3.4e-65;

Matches 163; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

125 NSNGALCHPPLVYNNHNTDCTSEGRDNNMKCGTTQYVADQKFGCPMAAHEICTTN 184

1 NSNGALCHPPLVYNNHNTDCTSEGRDNNMKCGTTQYVADQKFGCPMAAHEICTTN 60

185 EGVYVIRIGDQMDKQDMHMRCTGVNGRGWTCIAVSQALDQCTIVDITVYNNVDTFHK 244

61 EGVYVIRIGDQMDKQDMHMRCTGVNGRGWTCIAVSQALDQCTIVDITVYNNVDTFHK 120

245 RHEBGMNLCTCFGGGRGKMKCDPVQDQDSEFTGTFTYQIGDSWEKTVHGVYQCYG 304

121 RHEBGMNLCTCFGGGRGKMKCDPVQDQDSEFTGTFTYQIGDSWEKTVHGVYQCYG 180

305 IGEWHCOPLO 314

181 IGEWHCOPLO 190

RESULT 6

A53796

gelatinase B (EC 3.4.24.35), precursor - rabbit

N/Alternate names: 92K matrix metalloproteinase; 92K type IV collagenase; matrix metallo

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A53796; A55398

R/Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Egi

J. Biol. Chem. 269, 15006-15009, 1994

A/Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.

A/Reference number: A53796; PMID:94253056; PMID:8195136

A/Accession: A53796

A/Molecule type: mRNA

A/Residues: 1707 <TEZ>

A/Cross-references: GB:D26514; NID:9499372; PIRN:BA05520.1; PID:9499373

A/Experimental source: osteoclasts

R/Finl, M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Mody, M.K.; Girard, M.T.; R

J. Biol. Chem. 269, 28620-28628, 1994

A/Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and AP2 in cel

A/Reference number: A55398; PMID:95050662; PMID:7961810

A/Accession: A55398

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-75, 'P', '77-99', 'ASR', '103-171 <FIN>

A/Cross-references: GB:L36050; NID:9535714; PIRN:AAA64358.1; PID:9535715

C/Genetics: 46/3, 124/2

A/Intons: 46/3, 124/2

C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C/Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-106/Domain: activation peptide #status predicted <PRO>

F:107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>
F:220-271/Domain: fibronectin type II repeat homology <2F2>
F:288-329/Domain: fibronectin type II repeat homology <2F8>
F:347-388/Domain: fibronectin type II repeat homology <2F1>
F:510-704/Domain: hemopexin repeat homology <PXX>
F:88-120,127/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:402/Active site: Glu #status predicted

Query Match 19.8%; Score 396.5; DB 1; Length 707;
Best Local Similarity 45.4%; Pred. No. 3.1e-22;
Matches 79; Conservative 23; Mismatches 49; Indels 23; Gaps 6;

Qy 16 YGHCVTDSGVVSYGMOWLKTQGNKMLCTCIANGVSCQETAVIQTGYGNSGEPVLPF 75
Db 241 YTACTTGG--RSDGMAMCSTTADYD--TDRRFGFCSEHLVYQ--DGNMDKRCPEPF 292
Qy 76 TYNGRTYSCCTTEGRDGHLMCSTTSNYEQDKYSFC--TDHYLVVOTRGNSNGALCH 132
Db 293 IFQGRITYSACTTDRSDGRHWCATTASDYDKLXGFCPTRADSTVY---CGNSAGELCV 348
Qy 133 PPFVLYNNHNYTDCTSEGRDMKMGCTTQNYDADOKSEFCF-----MAHE 178
Db 349 PPFVFLGKRYSSCTSEGRDRMLWCATTASNFDSDKMGCFDCKGYSFLVAHE 402

RESULT 7

JC4364

gelatinase B (EC 3.4.24.35) precursor - rat

N:Alternate names: 92-kDa type IV collagenase; matrix metalloproteinase 9 (MMP9)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999

C/Accession: JC4364

R:Okada, A.; Santavirta, M.; Baeset, P.

Gene 164, 317-321, 1995.

A:Title: The cDNA cloning and expression of the gene encoding rat gelatinase B.

A:Reference number: JC4364; MUID:96069602; PMID:7590350

A/Accession: JC4364

A/Molecule type: mRNA

A:Residues: 1-708 <OKA>

A:Cross-references: CB:U24441; NID:g1173505; PIDN:AAA9911.1; PID:g1173506

A:Experimental source: Skin wounds

C/Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzyme.

C/Genetics:

A:Gene: gelB

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-708/Product: progelatinase B #status predicted <PRO>

F:25-107/Domain: activation peptide #status predicted <ACT>

F:108-708/Product: gelatinase B #status predicted <MAT>

F:214-389/Region: collagen binding #status predicted

F:231-272/Domain: fibronectin type II repeat homology <2F1>

F:289-310/Domain: fibronectin type II repeat homology <2F2>

F:348-389/Domain: fibronectin type II repeat homology <2F3>

F:514-707/Domain: hemopexin repeat homology <PXX>

F:39,121/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted

F:403/Active site: Glu #status predicted

F:519-707/Diulfide bonds: #status predicted

Query Match 19.8%; Score 393; DB 2; Length 708;
Best Local Similarity 31.8%; Pred. No. 5.7e-22;
Matches 98; Conservative 35; Mismatches 107; Indels 68; Gaps 12;

Qy 47 LGNGVSCQETAVIQTGYGNSGEPVLPFTYNGRTYSCCTTEGRDGHLMCSTTSNYEQD 106
Db 213 LGKG-----AVPTTFGNANGACHPFTFEGRSYLSCTTDGKNDGKPMCTTADYDPTD 266
Qy 107 QKYSFCTDHTVTVOTRGNSNGALCHPFLYNNHNYTDCTSEGRDMKMGCTTQNYDAD 166

Db 267 RKYGFPCSEN--LYTEHGNDGKRCVPPFIFBGHSYACTTKGRSDGRVCATTANYPD 324
Qy 167 OKFGFCMAAHEELCTTNE--GVM-----YHIGDQWDQOHMGHMRCTCGNGR--GEWT 218
Db 325 KLYGFCPTRADYDTVYTGNSGKMGCVPPFVFGKYS-----CTGEGSDRLW 373
Qy 219 CIAYSQD---RDQCIVDITVNVNDFPKRHEEGHMLNCTCFQGRGRWKCDPVQOCDS 275
Db 374 CATTSNFDADKKMGFCFDQGYSL--FLVAHEFGHALG-----LDHSSVP 416
Qy 276 ET-----GTRYQIDSMKRYVGRYQCYGKRGIGWHQPLQTPYSSGSPVVFPTTET 330
Db 417 EALYPMYHYHEDSPLHEDDIKGIQ---HDYGRG-----SKDPPRPATYAA 460
Qy 331 PSONSHP 338
Db 461 EPQTPAP 468

RESULT 8

S70365

gelatinase A (EC 3.4.24.24) precursor - rabbit

N:Alternate names: matrix metalloproteinase-2; type IV collagenase

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C/Accession: S70365

R:Matsumoto, S.; Katoh, M.; Watanabe, T.; Masuno, Y.

Biochim. Biophys. Acta 1307, 137-139, 1996

A:Title: Molecular cloning of rabbit matrix metalloproteinase-2 and its broad expression

A:Reference number: S70365; MUID:96283805; PMID:8679695

A/Accession: S70365

A:Status: preliminary

A/Molecule type: mRNA

A:Residues: 1-662 <MAT>

A:Cross-references: EMBL:D63579; NID:g944816; PIDN:BAA09796.1; PID:g944817

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:233-274/Domain: fibronectin type II repeat homology <2F1>

F:291-332/Domain: fibronectin type II repeat homology <2F2>

F:349-390/Domain: fibronectin type II repeat homology <2F3>

F:465-662/Domain: hemopexin repeat homology <PXX>

F:102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted

F:404/Active site: Glu #status predicted

Query Match 19.3%; Score 386.5; DB 2; Length 662;
Best Local Similarity 38.8%; Pred. No. 1.6e-21;
Matches 80; Conservative 29; Mismatches 76; Indels 21; Gaps 6;

Qy 55 ETAVTQTYGNSNGEPVLPFTYNGRTYSCCTTEGRDGHLMCSTTSNYEQDKYSFCTD 114
Db 217 EGVYRKYKYGADGELCKPFLPNKGYTCTDTGRSDGLMCKSTTTFKDKGYGTC-P 275
Qy 115 HTVLVOTRGNSNGALCHPFLYNNHNYTDCTSEGRDMKMGCTTQNYDADOKFGFCPM 174
Db 276 HEALF-TMGGNADQPCPKPFRFGTSYSTGTEGRDGYRWGCTTDDYDRDKKYGCP 334
Qy 175 AAHEICTTNEG-----MTRIGDQMKQDMGMHMRCTGVNGRGWTCLA---YGQLR 226
Db 335 TAMSITGNSGAPCVPPFTFLGKYES-----CTAGRGDGMKWCATSTNYDDDR 385
Qy 227 DQCIVDITVNVNDFPKRHEEGHML 252
Db 386 KWGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 9

A42496

gelatinase A (EC 3.4.24.24) precursor - mouse

N:Alternate names: collagenase type IV, 72K

C:Species: Mus musculus (house mouse)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999

C/Accession: A42496
 R.Reponen, P.; Sahlborg, C.; Huhtala, P.; Hurekainen, T.; Thestleff, I.; Trygsvaason, K.
 J. Biol. Chem. 267, 7856-7862, 1992
 A>Title: Molecular cloning of murine 72-kDa type IV collagenase and its expression during
 A/Reference number: A42496; PMID:92218452; PMID:1373140
 A/Accession: A42496
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-662 <REP>
 A/Cross-references: GB:M84324, NID:9198465, PIDN:AAA9338.1, PID:9198466
 A/Note: sequence extracted from NCBI backbone (NCBI:96943, NCBI:96945)
 C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:233-274/Domain: fibronectin type II repeat homology <2R1>
 F:291-332/Domain: fibronectin type II repeat homology <2R1>
 F:349-390/Domain: fibronectin type II repeat homology <2R5>
 F:465-662/Domain: hemopexin repeat homology <2P5>
 F:102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:404/Active site: Glu #status predicted

Query Match 19.3%; Score 385.5; DB 2; Length 662;
 Best Local Similarity 38.8%; Pred. No. 1.9e-21;
 Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVVQTGNSNGEPCVLPFTYNGRTFYSCTEGRODHLWCSSTSYEODKYSFCD 114
 DB 21 EQQVAVKYGNDGECYCKPFLFNGREYSSCTDGRSDGFLWCSSTYNEKDGKGF-C-P 275
 QY 115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDMMKMGCTTONTADQKFGFCPM 174
 DB 276 HNALF-TMGGNADGQCKPFRFGTSYNSCTTEGTDGRMGCTTEDYDRDKKGFCE 334
 QY 175 AAHEBICITTEGV----MYRIGDQMDKQHDGMMRCTCVNGSGEWTGIA--YSQR 226
 DB 335 TMSVTVGNSGEGAPCVFPFTFLGNKYS-----CTSGRNDGKWKVCAATTNYDDDR 385
 QY 227 DDCIYDDITVYNNVDFHKKRHEBGM 252
 DB 386 KMGFCPDGYSL--FLVAABEFGHAM 409

RESULT 10
 S34780
 gelatinase A (EC 3.4.24.24) precursor - rat
 N/Alternate names: collagenase type IV
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 22-Jun-1999
 C/Accession: S34780, S32525
 R.Lovett, D.H.
 submitted to the EMBL Data Library, June 1993
 A/Reference number: S34780
 A/Accession: S34780
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-662 <LOV>
 A/Cross-references: EMBL:X71466, NID:9311750, PIDN:CAA5083.1, PID:9854415
 R.Marti, H.P.; McNeill, L.; Davies, M.; Martin, J.; Lovett, D.H.
 Biochem. J. 291, 441-446, 1993
 A>Title: Homology cloning of rat 72 kDa type IV collagenase: cytokine and second-messeng
 A/Reference number: S32525, PMID:93249363, PMID:7916617
 A/Accession: S32525
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'R', 27-662 <MAR>
 A/Cross-references: EMBL:X71466
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:233-274/Domain: fibronectin type II repeat homology <2R1>
 F:291-332/Domain: fibronectin type II repeat homology <2R1>
 F:349-390/Domain: fibronectin type II repeat homology <2R5>
 F:465-662/Domain: hemopexin repeat homology <2P5>
 F:102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
 F:404/Active site: Glu #status predicted

Query Match 19.3%; Score 385.5; DB 2; Length 662;
 Best Local Similarity 38.8%; Pred. No. 1.9e-21;
 Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVVQTGNSNGEPCVLPFTYNGRTFYSCTEGRODHLWCSSTSYEODKYSFCD 114
 DB 21 EQQVAVKYGNDGECYCKPFLFNGREYSSCTDGRSDGFLWCSSTYNEKDGKGF-C-P 275
 QY 115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDMMKMGCTTONTADQKFGFCPM 174
 DB 276 HNALF-TMGGNADGQCKPFRFGTSYNSCTTEGTDGRMGCTTEDYDRDKKGFCE 334
 QY 175 AAHEBICITTEGV----MYRIGDQMDKQHDGMMRCTCVNGSGEWTGIA--YSQR 226
 DB 335 TMSVTVGNSGEGAPCVFPFTFLGNKYS-----CTSGRNDGKWKVCAATTNYDDDR 385
 QY 227 DDCIYDDITVYNNVDFHKKRHEBGM 252
 DB 386 KMGFCPDGYSL--FLVAABEFGHAM 409

RESULT 11
 A28153
 gelatinase A (EC 3.4.24.24) precursor - human
 N/Alternate names: collagenase type IV; matrix metalloproteinase 2 (MMP2); progelatinase
 C/Species: Homo sapiens (man)
 C/Date: 28-Aug-1989 #sequence_revision 07-Jul-1995 #text_change 18-Jun-1999
 C/Accession: A28153; A34202; A42225; A60187; S13658; S34336; A1480; S4432; A61498; S55
 R.Collier, I.E.; Wilhelm, S.M.; Eissen, A.Z.; Warner, B.L.; Grant, G.A.; Seltzer, J.L.; K
 J. Biol. Chem. 263, 6579-6587, 1988
 A>Title: H-ras oncogene-transformed human bronchial epithelial cells (TBE-1) secrete a si
 A/Reference number: A28153; PMID:88198218; PMID:2834383
 A/Accession: A28153
 A:Molecule type: mRNA
 A:Residues: 30-660 <COL>
 A/Cross-references: GB:J03210, NID:9180670, PIDN:AAA5701.1, PID:9180671
 R.Huhtala, P.; Eddy, R.L.; Fan, Y.S.; Byers, M.G.; Shows, T.B.; Trygsvaason, K.
 Genomics 6, 554-559, 1990
 A>Title: Completion of the primary structure of the human type IV collagenase preprocenzym
 A/Reference number: A34202; PMID:90228972; PMID:2158484
 A/Accession: A34202
 A:Molecule type: DNA
 A:Residues: 1-51 <HU2>
 A/Cross-references: GB:M33789, NID:9180600, PIDN:AAA52027.1, PID:9180601
 R.Huhtala, P.; Chow, L.T.; Trygsvaason, K.
 J. Biol. Chem. 265, 11077-11082, 1990
 A>Title: Structure of the human type IV collagenase gene.
 A/Reference number: A42225; PMID:90293047; PMID:2162831
 A/Accession: A42225
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-51;220-393 <HUH>
 A/Cross-references: GB:M55593; GB:J05471, NID:9180614, PIDN:AAA52028.1, PID:9180616
 A/Note: neither the complete amino acid nor the complete nucleotide sequence is given in
 R.Frisch, S.M.; Reich, R.; Collier, I.E.; Genrich, L.T.; Martin, G.; Goldberg, G.I.
 Oncogene 5, 75-83, 1990
 A>Title: Adenovirus E1A represses protease gene expression and inhibits metastasis of hum
 A/Reference number: A60187; PMID:90206614; PMID:2157183
 A/Accession: A60187
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-58 <FRI>
 R.Okada, Y.; Morimoto, T.; Enghild, J.J.; Suzuki, K.; Yasui, A.; Nakanishi, I.; Salvesen,
 Eur. J. Biochem. 194, 721-730, 1990
 A>Title: Matrix metalloproteinase 2 from human rheumatoid synovial fibroblasts. Purificat
 A/Reference number: S13858; PMID:91099551, PMID:2269296
 A/Accession: S13858
 A:Molecule type: protein
 A:Residues: 30-45;110-124 <OKA>
 R.Crabbe, T.; Ioannou, C.; Docherty, A.J.P.

Eur. J. Biochem. 218, 431-438, 1993
A:Title: Human progelatinase A can be activated by autolysis at a rate that is concentrated
A:Reference number: S39436; MUID:94094834; PMID:8269931
A:Accession: S39436
A:Molecule type: protein
R:Residues: 30-44/444-456 <CR2>
R:Stetler-Stevenson, W.G.; Krutzsch, H.C.; Wachter, M.P.; Margulies, I.M.K.; Liotta, L.A.
J. Biol. Chem. 264, 1353-1356, 1989
A:Title: The activation of human type IV collagenase proenzyme. Sequence identification
A:Reference number: A31480; MUID:89109136; PMID:2536363
A:Accession: A31480
A:Molecule type: protein
R:Residues: 110-123 <STB>
R:Crabbe, T.; Smith, B.; O'Connell, J.; Docherty, A.
FEBS Lett. 345, 14-16, 1994
A:Title: Human progelatinase A can be activated by matrixlysin.
A:Reference number: S44432; MUID:94252395; PMID:8194591
A:Accession: S44432
A:Molecule type: protein
A:Residues: 110-115 <CRA>
R:Brown, D.; Chwa, M.; Escobar, M.; Kenney, M.C.
Exp. Eye Res. 52, 5-16, 1991
A:Title: Characterization of the major matrix degrading metalloproteinase of human corne
A:Reference number: A61498; MUID:91330998; PMID:1868885
A:Accession: A61498
A:Molecule type: protein
A:Residues: 'X', '31', 'X', '33-46', 'X', '48-50', 'Q' <BRO>
A:Experimental source: corneal stroma
R:Ich, Y.; Blinner, S.; Nagase, H.
Biochem. J. 308, 645-651, 1995
A:Title: Steps involved in activation of the complex of pro-matrix metalloproteinase 2
A:Reference number: S55327; MUID:95290003; PMID:7772054
A:Accession: S55327
A:Molecule type: protein
A:Residues: 110-114 <ITO>
C:Genetics:
A:Gene: GDB:MMP2, CLG4; CLG4A
A:Cross-References: GDB:120592; OMIM:120360
A:Map position: 16q13-16q13
A:Insertions: 51/3; 127/2; 178/1; 220/1; 278/1; 336/1; 394/1; 446/1; 491/2; 537/1; 590/2; 6
C:Function:
A:Description: proteolytic cleavage of gelatin type I and collagen types IV, V, VII, and
C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-29/Domin: signal sequence #status predicted <SIG>
F:30-660/Product: progelatinase A #status predicted <PRO>
F:30-109/Domin: activation peptide #status predicted <ACT>
F:70-219,394-446/Domin: matrix metalloproteinase homology #status atypical <MMP>
F:110-660/Product: gelatinase A #status predicted <MAT>
F:233-390/Region: collagen binding #status predicted
F:233-374/Domin: fibronectin type II repeat homology <2F1>
F:291-332/Domin: fibronectin type II repeat homology <2F2>
F:349-390/Domin: fibronectin type II repeat homology <2F3>
F:463-660/Domin: hemopexin repeat homology <PXN>
F:102,403,407,413/Binding site: zinc, catalytic (His, His, His, His) (inhibited) #status
F:403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F:404/Active site: Glu #status predicted
F:469-660/Dissulfide bonds: #status predicted
F:573,642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 382.5; DB 1; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.2e-21;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQYVGNSEBPCVLPFTYNGRFRFVSTTSGRQDGHLMWSTTSNYEDOKYSCTD 114
DB 217 EGVVARKYKYNADSEYCKPFLFNGKEVNSCTDGRSGFLWCGSTYVNFEDGKYGFC-P 275

QY 115 HTVLVQTRGNSGALCHFPFLYNNHNYTDCSEGRDNMKWCGTTONYDADOKFGFCPM 174
DB 276 HEALF-TMGNAEBOQPCFPFRFOGTSTSDCTTGRDYGKWCCTTEDYDOKKYGFCPE 334

QY 175 AAHEICTTNEG-V-----MYRIGDQMDKQHDGMHMRCTCVNGRGSEWTCIA---YSQLR 226

DB 335 TAMSTVGNSEBAPCVFPFFFLNKKYBS-----CTSAGRSDBGKWCATTANYDDDR 385
QY 227 DQCIVDITVNDTFPKHREBGMHL 252
DB 386 KWGFCPDQYSL--FLVAHAEFGHAM 409

RESULT 12
S46492
gelatinase A (EC 3.4.24.24) precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S46492
R:Aimes, R.T.; French, D.L.; Quigley, J.P.
Biochem. J. 300, 729-736, 1994
A:Title: Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from chicken embryo fi
A:Reference number: S46492; MUID:94280397; PMID:8010954
A:Accession: S46492
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-663 <AIM>
A:Cross-References: EMBL:U07775; NID:G504475; PUD:AAA19596.1; PID:G504476
A>Note: in the authors' translation 205-Asp is shown after residue 201 and, consequently,
C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:67-216,391-443/Domin: matrix metalloproteinase homology #status atypical <MMP>
F:230-271/Domin: fibronectin type II repeat homology <2F1>
F:268-329/Domin: fibronectin type II repeat homology <2F2>
F:346-387/Domin: fibronectin type II repeat homology <2F3>
F:466-663/Domin: hemopexin repeat homology <PXN>
F:99,400,404,410/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status i
F:400,404,410/Binding site: zinc, catalytic (His) (active) #status predicted
F:401/Active site: Glu #status predicted

Query Match 19.1%; Score 382.5; DB 1; Length 663;
Best Local Similarity 37.0%; Pred. No. 3.3e-21;
Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;

QY 55 ETAVTQYVGNSEBPCVLPFTYNGRFRFVSTTSGRQDGHLMWSTTSNYEDOKYSCTD 114
DB 214 EGVVARKYKYNADSEYCKPFLFNGKEVNSCTDAGRNDGLWCSITDOPADGKYGFCPH 273

QY 115 HTVLVQTRGNSGALCHFPFLYNNHNYTDCSEGRDNMKWCGTTONYDADOKFGFCPM 174
DB 274 ESLE--TMGNGDGOQPCFPFKQGGSYDQCTTEGRDYGKWCCTTEDYDOKKYGFCPE 331

QY 175 AAHEICTTNEG-V-----MYRIGDQMDKQHDGMHMRCTCVNGRGSEWTCIASQLRDQ- 228
DB 332 TAMSTVGNSEBAPCVFPFFFLNKKYDS-----CTSAGRNDGLWCASTSSSYDDDR 382

QY 229 ----CIVDDITVNDTFPKHREBGMHL 252
DB 383 KWGFC--PDQYSL--FLVAHAEFGHAM 406

RESULT 13
S62907
gelatinase B (EC 3.4.24.35) precursor - rat
N:Alternate names: collagenase type IV
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 30-Sep-2001
C:Accession: S62907; S72371
R:Xi, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 382, 285-288, 1996
A:Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinar
A:Reference number: S62907; MUID:96184505; PMID:8605986
A:Accession: S62907
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-708 <XIA>
A:Cross-References: EMBL:U36476
R:Feng, L.

submitted to the EMBL Data Library, September 1995

A:Reference number: S72371

A:Accession: S72371

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127, 'S', 129-708 <FEN>

A:Cross-references: EMBL:U6476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-107/Domain: propeptide #status predicted <PRO>

F:58-217,393-445/Domain: activation peptide #status predicted <ACT>

F:108-708/Region: gelatinase A #status predicted <MAT>

F:214-389/Region: collagen binding #status predicted

F:231-272/Domain: fibronectin type II repeat homology <2F1>

F:289-330/Domain: fibronectin type II repeat homology <2F2>

F:348-389/Domain: fibronectin type II repeat homology <2F3>

F:514-707/Domain: hemopexin repeat homology <PXN>

F:100-402,406,412/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted

F:403/Active site: Glu #status predicted

F:519-707/Disulfide bonds: #status predicted

Query Match 19.1%; Score 382; DB 2; Length 708;

Best Local Similarity 38.1%; Pred. No. 3, Be-21;

Matches 82; Conservative 25; Mismatches 80; Indels 28; Gaps 7;

47 LGNGVSCQETAVYQYTGSGNSGEPVLPFTYNGRTFYSCCTEGRODGLWCSTTSNYEOD 106

213 LGKG-----AVPTYTGNGANGAPCHPFPFEGRSYLSCTTDGNDGKPMCGTTADYD 266

107 QKXSFCTDHTVLTOTRGSGNSGALCHPFLNNHNTDCTSEGRDMMKCGTTONYDAD 166

267 RKYGFCSEN--LYTEGNDGKRCVPPFIEGHSYSACTTKGSDRYWCATTANYDOD 324

167 QKGFCEPMAAHEICTTNE-GVM-----YRIGDQWDQHMGMRCCTCGNGSGEWTCI 220

325 KAGGFCETRADVYVTGNSGEMKVPFPVPLGKQYS-----TCTSEGRSDGRLMCA 375

221 AYSQL--RDQCIYDITTYNVNDFHKKHEGHML 252

376 TTSNFADKKMKGFCPDQGYSL--FLVAHEFGHML 408

Db

RESULT 14

152580

gelatinase B (EC 3.4.24.35) precursor - mouse

N:Alternate names: collagenase type IV

C:Species: Mus sp. (mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: 152580

R:Grabert, T.; Johnston, J.; Berliner, N.

Blood 82, 3193-3197, 1993

A:Title: Cloning and expression of the cDNA encoding mouse neutrophil gelatinase: demon

A:Reference number: 152580; MUID:94033534; PMID:81291207

A:Accession: 152580

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-730 <RES>

A:Cross-references: GB:S67830; NID:9460863; PIDN:AAB28942.1; PID:9460864

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:230-271/Domain: fibronectin type II repeat homology <2F1>

F:288-329/Domain: fibronectin type II repeat homology <2F2>

F:347-388/Domain: fibronectin type II repeat homology <2F3>

F:529-729/Domain: hemopexin repeat homology <PXN>

F:100,401,405,411/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted

F:402/Active site: Glu #status predicted

Query Match 19.1%; Score 382; DB 1; Length 730;

Best Local Similarity 40.1%; Pred. No. 3, 9e-21;

Matches 79; Conservative 26; Mismatches 52; Indels 40; Gaps 8;

16 YGHCTDSDGVVSVGMQWLT-----QGNQMCLCTGANGVSCQETAVYQYTGSGNSGEP 70

241 YSACTTDG--RNDGFPWCSTADYDQDFGFCP-----SERLYT--HNGEGKP 287

71 CVLPFTYNGRTFYSCCTEGRODGLWCSTTSNYEODQKYSFC--IDHTVLTOTRGSGNS 127

288 CVLPFIEGHSYSACTTKGSDRYWCATTANYDOKLYFCCTRADYATV-----GQNSA 343

128 GALCHPFLNNHNTDCTSEGRDMMKCGTTONYDADQKFCP-----MAAHE- 178

344 GELCVPPFPVPLGKQYSCTSDGRDGLMCAITSNFTDCKMGFCPDQGYSLFLVAHEF 403

179 -----EICTNKGWY 189

404 GHALGDHSSVPEALMY 420

Db

RESULT 15

JC1456

gelatinase B (EC 3.4.24.35) precursor - mouse

N:Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C:Accession: JC1456; S39525; S39526; I48296; S38654

R:Tanaka, H.; Hojo, K.; Yoshida, H.; Yoshida, T.; Sugita, K.

Biochem. Biophys. Res. Commun. 190, 732-740, 1993

A:Title: Molecular cloning and expression of the mouse 105-kDa gelatinase cDNA.

A:Reference number: JC1456; MUID:93176173; PMID:8382489

A:Accession: JC1456

A:Molecule type: mRNA

A:Residues: 1-730 <TRAN>

A:Cross-references: DBJ:D12712; NID:9286079; PIDN:BA02208.1; PID:9286080

R:Maure, S.; Nye, G.; Fiten, P.; van Damme, J.; Opdenacker, G.

Eur. J. Biochem. 218, 129-141, 1993

A:Title: Mouse gelatinase B. cDNA cloning, regulation of expression and glycosylation in

A:Reference number: S39525; MUID:94062823; PMID:8243459

A:Accession: S39525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-638, 'L', 640-730 <MAS>

A:Cross-references: EMBL:X72794; NID:9433432; PIDN:CA51314.1; PID:9433433

A:Accession: S39526

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 133-513, 'A', 515-710, 'P', 712-730 <MA2>

A:Cross-references: EMBL:X72795; NID:9433434; PIDN:CA51315.1; PID:9433435

R:Reponen, P.; Sahlborg, C.; Munaut, C.; Thesleff, I.; Tytgvaason, K.

J. Cell Biol. 124, 1091-1102, 1994

A:Title: High expression of 92-kD type IV collagenase (gelatinase B) in the osteoclast li

A:Reference number: A54476; MUID:94179406; PMID:8132709

A:Accession: I48296

A:Molecule type: mRNA

A:Residues: 1-513, 'A', 515-710, 'P', 712-730 <RES>

A:Cross-references: EMBL:Z27231; NID:9415980; PIDN:CA581745.1; PID:9415981

C:Gene: C14B

A:Intons: 47/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 555/2; 602/1; 652/2; 6

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase,

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-730/Region: progelatinase A #status predicted <PRO>

F:108-330/Region: activation peptide #status predicted <ACT>

F:213-388/Region: collagen binding #status predicted <MAT>

F:230-271/Domain: fibronectin type II repeat homology <2F1>

F:288-329/Domain: fibronectin type II repeat homology <2F2>

F:347-388/Domain: fibronectin type II repeat homology <2F3>

F:529-729/Region: hemopexin repeat homology <PXN>

F:100,401,405,411/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted

F:402/Active site: Glu #status predicted
F:534-729/Disulfide bonds: #status predicted

Query Match 19.1%; Score 382; DB 2; Length 730;
Best Local Similarity 40.1%; Pred. No. 3.9e-21;
Matches 79; Conservative 26; Mismatches 52; Indels 40; Gaps 8;

QY 16 YGHCVTDSGVVSVGMQWLT-----QGNKQMLCTCLGNVSCQETAVTQTYGNSNGEP 70
Db 241 YSACTTDG---RNDGTPWCSTTADYDKDKFGFCP-----SERLYTE--HGNGEGKP 287
QY 71 CVLPETVNGRTFFYSCTTEGRDGHLMCSTSTSNYEDOKYSFC---TDHTVLVQTRGNSN 127
Db 288 CVPPPIFEGRSYSACTTGRSDGYRWCATTANYDQDKLYGFCPTFRVDATV---GNSA 343
QY 128 GALCHFPFLNNHNYTDCSTSEGRDNMKMGCTTONYADADOKFGFCP-----MAHE- 178
Db 344 GELCVFPFVFLGKQYSSCTSDGRDRGLMCATTSNFDTKKMGFCPDQGYSLFLVAHEF 403
QY 179 -----EICTTNEGVMY 189
Db 404 GHALGLDHSVPEALMY 420

Search completed: November 28, 2003, 15:02:08
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 17 Seconds

(without alignments)
948.833 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002

Sequence: 1 MAAYVQPPHPQPPYGHCV.....EVPITETPSPNSHPICWLE 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1984	99.1	2386	1	F1NC_HUMAN
2	1927	96.3	2265	1	F1NC_BOVIN
3	1877	93.8	2477	1	F1NC_RAT
4	1591	79.5	2481	1	F1NC_XENTLA
5	961	48.0	190	1	F1NC_NOVI
6	396.5	19.8	707	1	MM09_RABIT
7	386.5	19.3	662	1	MM02_RABIT
8	385.5	19.3	662	1	MM02_MOUSE
9	385.5	19.3	662	1	MM02_RAT
10	382.5	19.1	660	1	MM02_HUMAN
11	382.5	19.1	663	1	MM02_CHICK
12	382	19.1	708	1	MM09_RAT
13	382	19.1	730	1	MM09_MOUSE
14	381	19.0	712	1	MM09_BOVIN
15	374	18.7	707	1	MM09_HUMAN
16	373	18.6	2477	1	F1NC_MOUSE
17	364.5	18.2	704	1	MM09_CANFA
18	291	14.5	1256	1	F1NC_CHICK
19	210	10.5	1328	1	F1NC_PLEWMA
20	200.5	10.0	522	1	F1NC_HORSE
21	196.5	9.8	522	1	F1NC_CANFA
22	195.5	9.8	1463	1	PA2R_BOVIN
23	195	9.7	1463	1	PA2R_MOUSE
24	193	9.6	1456	1	MANR_HUMAN
25	190.5	9.5	1458	1	SPI_HORSE
26	189.5	9.5	1458	1	PA2R_RABIT
27	178.5	8.9	183	1	SEPA_BOVIN
28	175.5	8.8	130	1	PBI_PIG
29	170	8.5	655	1	HGFAL_HUMAN
30	170	8.5	794	1	SEIL_HUMAN
31	165	8.2	615	1	FA12_HUMAN
32	164.5	8.2	134	1	SFP1_BOVIN
33	164.5	8.2	140	1	SFP3_BOVIN

ALIGNMENTS

34	163	8.1	790	1	SEIL_MOUSE
35	159	7.9	2483	1	MPRI_MOUSE
36	156.5	7.8	2491	1	MPRI_HUMAN
37	156.5	7.8	2489	1	MPRI_BOVIN
38	154	7.7	593	1	FA12_BOVIN
39	144	7.2	603	1	FA12_CANFA
40	129.5	6.5	611	1	LEM2_MOUSE
41	125	6.2	551	1	LEM2_RABIT
42	125	6.2	3712	1	LMA_DROME
43	123.5	6.2	4655	1	LRE2_HUMAN
44	123	6.1	1202	1	JAG2_RAT
45	122.5	6.1	2215	1	SORL_MOUSE

RESULT 1	F1NC_HUMAN	STANDARD;	PRT; 2386 AA.
ID	P02751; O14326; Q9H1B8;		
AC	21-JUL-1986 (Rel. 01, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).		
GN	FN1 OR FN.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE OF 1-38 FROM N.A.		
RX	MEDLINE=87030880; PubMed=3770189;		
RA	Gutman A., Yamada K.M., Kornblint A.R.;		
RT	"Human fibronectin is synthesized as a pre-propolypeptide.";		
RL	FEBS Lett. 207:145-148(1986).		
RN	[2]		
RP	SEQUENCE OF 1-49 FROM N.A.		
RX	MEDLINE=87175578; PubMed=3031656;		
RA	Dean D.C., Bowles C.L., Bourgeois S.;		
RT	"Cloning and analysis of the promoter region of the human fibronectin gene.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).		
RN	[3]		
RP	SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.		
RX	MEDLINE=85284965; PubMed=29292939;		
RA	Kornblint A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;		
RT	"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";		
RL	EMBO J. 4:1755-1759(1985).		
RN	[4]		
RP	SEQUENCE OF 973-2081 AND 2113-2386 FROM N.A.		
RX	MEDLINE=84272258; PubMed=6462919;		
RA	Kornblint A.R., Vibe-Pedersen K., Baralle F.E.;		
RT	"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";		
RL	Nucleic Acids Res. 12:5853-5868(1984).		
RN	[5]		
RP	SEQUENCE OF 1594-2386 FROM N.A.		
RX	MEDLINE=85280409; PubMed=292573;		
RA	Bernard M.P., Kolbe M., Weil D., Chu M.-L.;		
RT	"Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";		
RL	Biochemistry 24:2698-2704(1985).		
RN	[6]		
RP	SEQUENCE OF 32-290.		
RX	MEDLINE=84032463; PubMed=6630202;		
RA	Garcia-Pardo A., Pearlstein E., Frangione B.;		
RT	"Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";		
RL	J. Biol. Chem. 258:12670-12674(1983).		
RN	[7]		

RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
in *Escherichia coli*.";
RL EMBO J. 5:2825-2830(1986).
RN
RP SEQUENCE OF 1441-1548.
RX MEDLINE=82265604; PubMed=7050098;
RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
RT "The cell attachment domain of fibronectin. Determination of the
primary structure.";
RL J. Biol. Chem. 257:9593-9597(1982).
RN
RP SEQUENCE OF 1434-1537 FROM N.A.
RX MEDLINE=83290929; PubMed=6688418;
RA Oldberg A., Linney E., Ruoslahti E.;
RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
the cell attachment domain in human fibronectin.";
RL J. Biol. Chem. 258:10193-10196(1983).
RN
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=86111901; PubMed=3003095;
RA Oldberg A., Ruoslahti E.;
RT "Evolution of the fibronectin gene. Exon structure of cell attachment
domain.";
RL J. Biol. Chem. 261:2113-2116(1986).
RN
RP SEQUENCE OF 1712-1739 FROM N.A.
RX MEDLINE=87026579; PubMed=3021206;
RA Setiguchi K., Kios A.M., Kirsch K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
different messenger RNAs possibly encoding the alpha and beta
subunits of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Schor S.L., Schor A.M., Seneviratne K., Kay R., Ellis I., Baillie R.,
RA Clausen J.;
RT "Migration stimulating factor (MSF): a novel transcription variant of
the fibronectin gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
RP SUBFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN
RP FBLN1-BINDING SITE.
RX PubMed=1400330;
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
RA Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
region of fibronectin.";
RL J. Biol. Chem. 267:20120-20125(1992).
RN
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=95081153; PubMed=7989369;
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT "Further characterization of the NH2-terminal fibrin-binding site on
fibronectin.";
RL J. Biol. Chem. 269:31938-31945(1994).
RN
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=96069779; PubMed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking
site and the first type I module of fibronectin.";
RL Nat. Struct. Biol. 2:946-950(1995).
RN
RP STRUCTURE BY NMR OF 182-275.

RX MEDLINE=94141923; PubMed=8308892;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
RA Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with
fibrin binding activity.";
RL J. Mol. Biol. 235:1302-1311(1994).
RN
RP STRUCTURE BY NMR OF 406-464.
RX MEDLINE=98179558; PubMed=9514732;
RA Sticht H., Pickford A.R., Potts J.R., Campbell I.D.;
RT "Solution structure of the glycosylated second type 2 module of
fibronectin.";
RL J. Mol. Biol. 276:177-187(1998).
RN
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=9304665; PubMed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of
fibronectin: an insight into RGD-mediated interactions.";
RL Cell 71:671-678(1992).
RN
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=92162710; PubMed=1311202;
RA Baron M., Main A.L., Discolli P.C., Mardon H.J., Boyd J.,
RA Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type
III module of fibronectin.";
RL Biochemistry 31:2068-2073(1992).
RN
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1555.
RX MEDLINE=94166075; PubMed=9120886;
RA Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xiong N.-H.,
RA Ruoslahti E., Ely K.R.;
RT "Crystal structure of the tenth type III cell adhesion module of
human fibronectin.";
RL J. Mol. Biol. 236:1079-1092(1994).
RN
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.
RX MEDLINE=99177162; PubMed=10075919;
RA Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.I.;
RT "Crystal structure of a heparin- and integrin-binding segment of human
fibronectin.";
RL EMBO J. 18:1468-1479(1999).
RN
RP FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC
CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variants, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extent homodimers. Interacts with FBLN1.
CC
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P02751-1; Sequence=Displayed;
Name=2; Synonyms=MSF-FN70, Migration stimulation factor FN70;
IsoId=P02751-2; Sequence=VSP 003255, VSP 003256, VSP 003257;
CC
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC
CC -1- PTM: SULFATED.
CC
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC
CC -1- SIMILARITY: Contains 16 fibronectin type III domains.
CC
CC -----
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or send an email to license@isb-sib.ch).

Query Match 99.1%; Score 1984; DB 1; Length 2386;
Best Local Similarity 99.7%; Pred. No. 5,1e-156;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVYQPPHPPPPYCHVTDSGVVSVGMQWMLKTKGNKMLCTCLGNGVSCGEIATVOT 61
DB 291 AAVYQPPHPPPPYCHVTDSGVVSVGMQWMLKTKGNKMLCTCLGNGVSCGEIATVOT 350
QY 62 YGNGSGECVLPFTYNGRTFYCTEGRDGLHNCSTTSNRYDOKYSCFCDHTVLYOT 121
DB 351 YGNGSGECVLPFTYNGRTFYCTEGRDGLHNCSTTSNRYDOKYSCFCDHTVLYOT 410
QY 122 RGNGSGALCHPEFLNNHNYTDCSEGRDNKMGCTQNVADOKPFGCPMAHEBIC 181
DB 411 QGNGSGALCHPEFLNNHNYTDCSEGRDNKMGCTQNVADOKPFGCPMAHEBIC 470
QY 182 TTNEGVMYRIGDQWDKQHDGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDITVNVNDT 241
DB 471 TTNEGVMYRIGDQWDKQHDGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDITVNVNDT 530
QY 242 FKRHEEGHMLNCTCGGGRGKCPVDCDSEGTGTQIGDSWEKTVHGVRQCYCY 301
DB 531 FKRHEEGHMLNCTCGGGRGKCPVDCDSEGTGTQIGDSWEKTVHGVRQCYCY 590
QY 302 GRGIGMHCOPLQTPYSSGPVVFITTEPSPNSHPIDW 341
DB 591 GRGIGMHCOPLQTPYSSGPVVFITTEPSPNSHPIDW 630

RESULT 2
FINC BOVIN STANDARD; PRT; 2265 AA.

ID F1NC BOVIN STANDARD; PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibronectin (FN).
GN FNI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.B., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.",
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.B., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RT Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectin.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OSSONIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
TO A LESSER EXTEND HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=P07589-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES, CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 15 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00800; AAA0521.2; -.
CC PIR; A26452; FNBO.
CC HSSP; P02751; 2FN2.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR000083; Fibnrcn1.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR000562; FN Type II.
CC InterPro; IPR003962; FnIII_subd.
CC Pfam; PR00039; fnI; 12.
CC Pfam; PR00040; fn2; 2.
CC Pfam; PR00041; fn3; 15.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00014; FNTYPEIII.
CC ProDom; P0000995; FN Type II; 2.
CC SMART; SM00058; FN1_12.
CC SMART; SM00059; FN2; 2.
CC SMART; SM00060; FN3; 14.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS00023; FIBRONECTIN 2; 2.
CC PROSITE; PS01253; FIBRONECTIN 1; 12.
CC GlycoProtein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing;
CC Pyroliidone carboxylic acid.
CC MOD_RES 1 1
CC FT 21 241
FT DOMAIN 277 577
FT DNA_BIND 876 1141
FT DOMAIN 1236 1509
FT DOMAIN 1600 1870
FT DOMAIN 1991 2216
FT DOMAIN 19 59
FT DOMAIN 64 107
FT DOMAIN 108 151
FT DOMAIN 153 197
FT DOMAIN 198 242
FT DOMAIN 275 314
FT DOMAIN 314 373
FT DOMAIN 374 438
FT DOMAIN 437 480
FT DOMAIN 485 527
FT DOMAIN 528 571
FT DOMAIN 578 669
FT DOMAIN 688 778
FT DOMAIN 779 874
FT DOMAIN 875 964
FT DOMAIN 965 1054
FT DOMAIN 1055 1141
FT DOMAIN 1142 1234
FT DOMAIN 1235 1325
FT DOMAIN 1326 1415
CELL-ATTACHMENT.
HEPARIN-BINDING 2.
FIBRIN-BINDING 2.
FIBRONECTIN TYPE-I 1.
FIBRONECTIN TYPE-I 1.
FIBRONECTIN TYPE-I 2.
FIBRONECTIN TYPE-I 3.
FIBRONECTIN TYPE-I 4.
FIBRONECTIN TYPE-I 5.
FIBRONECTIN TYPE-I 6.
FIBRONECTIN TYPE-I 7.
FIBRONECTIN TYPE-I 8.
FIBRONECTIN TYPE-I 9.
FIBRONECTIN TYPE-II 1.
FIBRONECTIN TYPE-II 2.
FIBRONECTIN TYPE-II 3.
FIBRONECTIN TYPE-II 4.
FIBRONECTIN TYPE-II 5.
FIBRONECTIN TYPE-II 6.
FIBRONECTIN TYPE-II 7.
FIBRONECTIN TYPE-II 8.
FIBRONECTIN TYPE-II 9.

FT DOMAIN 1416 1509 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1510 1599 FIBRONECTIN TYPE-III 11. (EXTRA DOMAIN).
 FT DOMAIN 1600 1691 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1692 1780 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1781 1870 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1871 1990 CONNECTING STRAND 3 (CS-3) (V REGION).
 FT DOMAIN 1982 2061 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2062 2127 FIBRONECTIN TYPE-I 10.
 FT DOMAIN 2128 2170 FIBRONECTIN TYPE-I 11.
 FT DOMAIN 2172 2215 FIBRONECTIN TYPE-I 12.
 FT SITE 1493 1495 CELL ATTACHMENT SITE.
 FT DISULFID 21 47
 FT DISULFID 45 56
 FT DISULFID 66 94
 FT DISULFID 92 104
 FT DISULFID 110 138
 FT DISULFID 136 148
 FT DISULFID 155 184
 FT DISULFID 182 194
 FT DISULFID 200 229
 FT DISULFID 227 239
 FT DISULFID 277 304
 FT DISULFID 302 311
 FT DISULFID 329 355
 FT DISULFID 343 370
 FT DISULFID 389 415
 FT DISULFID 403 430
 FT DISULFID 439 467
 FT DISULFID 465 477
 FT DISULFID 487 514
 FT DISULFID 512 524
 FT DISULFID 530 558
 FT DISULFID 556 568
 FT DISULFID 2085 2114
 FT DISULFID 2112 2124
 FT DISULFID 2130 2157
 FT DISULFID 2155 2167
 FT DISULFID 2174 2200
 FT DISULFID 2198 2209
 FT DISULFID 2246 2246
 FT DISULFID 2250 2250
 FT MOD_RES 845 845
 FT MOD_RES 850 850
 FT CARBOHYD 399 399
 FT CARBOHYD 497 497
 FT CARBOHYD 511 511
 FT CARBOHYD 846 846
 FT CARBOHYD 976 976
 FT CARBOHYD 1213 1213
 FT CARBOHYD 1987 1987
 FT CARBOHYD 1943 1943
 FT CARBOHYD 1944 1944
 FT MOD_RES 2263 2263
 SQ SEQUENCE 2265 AA; 249557 MW; C2D21D486F498B5C CRC64;

Query Match 96.3%; Score 1927; DB 1; Length 2265;
 Best Local Similarity 96.5%; Pred. No. 2.5e-15;
 Matches 327; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 441 TNEGWMTRIGDQMDKQDHMGHMRCTCVGNGRGWTCVAYSQLRDCCIVDGITYNVNDTF 500
 Qy 243 HKRHEEGHMLNCTCFGGGRGWKCDPYDQCODSETGTFTYQIGSWEKYHGVRYQCYG 302
 Db 501 HKRHEEGHMLNCTCFGGGRGWKCDPYDQCODSETGTFTYQIGSWEKYHGVRYQCYG 560
 Qy 303 RGISEWHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 341
 Db 561 RGISEWHCOPLOTYPSSSGPVEVFITETPSQPNSHPIQW 599

RESULT 3
 FINE_RAT STANDARD; PRT; 2477 AA.
 AC P04937;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibrinectin precursor (FN).
 GN FN1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RX MEDLINE=88054951; PubMed=2445560;
 RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
 RT "Multiple sites of alternative splicing of the rat fibrinectin gene
 transcript.";
 RL EMBO J. 6:2573-2580(1987).
 RN [2]
 RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RX MEDLINE=88054950; PubMed=3119323;
 RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
 RT "Organization of the fibrinectin gene provides evidence for exon
 shuffling during evolution.";
 RL EMBO J. 6:2565-2572(1987).
 RN [3]
 RP SEQUENCE OF 1586-2477 FROM N.A.
 RX MEDLINE=84082067; PubMed=6317187;
 RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;
 RT "Three different fibrinectin mRNAs arise by alternative splicing
 within the coding region.";
 RL Cell 35:421-431(1983).
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 VARIANTS. CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 TO A LESSER EXTEND HOMODIMERS.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Each of the "extra domain" and the connecting strand 3
 CC are present in some forms of fibrinectin and absent in others;
 CC Name=1;
 CC IsoId=P04937-1; Sequence=Displayed;
 CC Name=2; Synonyms=FNII-13-lees;
 CC IsoId=P04937-2; Sequence=VSP_003258;
 CC Name=3; Synonyms=Lambda-RLF4-5;
 CC IsoId=P04937-3; Sequence=VSP_003259;
 CC Name=4; Synonyms=Lambda-RLF6;
 CC IsoId=P04937-4; Sequence=VSP_003260;
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC -1- PM: SULFATED (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 12 fibrinectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibrinectin type II domains.

CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL; X15906; CA34020.1; -;
 DR EMBL; L29191; AAA41166.1; -;
 DR EMBL; L29191; AAA41166.1; JOINED.
 DR EMBL; L29191; AAA41167.1; -;
 DR EMBL; L29191; AAA41167.1; JOINED.
 DR EMBL; L29191; AAA41168.1; -;
 DR EMBL; L00191; AAA41168.1; JOINED.
 DR EMBL; X05831; CAA29278.1; -;
 DR EMBL; X05832; CAA29279.1; -;
 DR EMBL; X05833; CAA29280.1; -;
 DR EMBL; X05834; CAA29281.1; -;
 DR EMBL; X05834; CAA29281.1; -;
 DR HSP; S14428; S14428.
 DR HSP; P02751; 1FBR.
 DR InterPro; IPRO06209; EGF like.
 DR InterPro; IPRO00083; Fibronctn.
 DR InterPro; IPRO03961; FN III.
 DR InterPro; IPRO00562; FN_type_II.
 DR InterPro; IPRO03962; FNIII_sdbd.
 DR Pfam; PF00039; fn1; 12.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 17.
 DR PRINTS; PR00013; FNTPR1.
 DR PRINTS; PR00014; FNTPR1.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 12.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 13.
 DR PROSITE; PS00023; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR GlycoProfile; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal.
 FT CHAIN 1 32
 FT SIGNAL 1 32
 FT DOMAIN 53 273 FIBRONECTIN.
 FT DOMAIN 308 608 FIBRIN- AND HEPARIN-BINDING 1.
 FT DVA BIND 906 1171 COLLAGEN-BINDING.
 FT DOMAIN 1357 1630
 FT DOMAIN 1811 2081 CELL-ATTACHMENT.
 FT DOMAIN 2296 2427 HEPARIN-BINDING 2.
 FT DOMAIN 51 91 FIBRIN-BINDING 2.
 FT DOMAIN 96 139 FIBRONECTIN TYPE-I 1.
 FT DOMAIN 140 183 FIBRONECTIN TYPE-I 2.
 FT DOMAIN 185 229 FIBRONECTIN TYPE-I 3.
 FT DOMAIN 230 274 FIBRONECTIN TYPE-I 4.
 FT DOMAIN 306 345 FIBRONECTIN TYPE-I 5.
 FT DOMAIN 345 404 FIBRONECTIN TYPE-I 6.
 FT DOMAIN 405 461 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 468 511 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 516 558 FIBRONECTIN TYPE-I 8.
 FT DOMAIN 559 602 FIBRONECTIN TYPE-I 9.
 FT DOMAIN 609 706 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 707 808 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 809 903 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 904 994 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 995 1084 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 1085 1172 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 1173 1264 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1265 1355 FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN 1).
 FT DOMAIN 1356 1446 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1447 1536 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1537 1630 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1631 1720 FIBRONECTIN TYPE-III 12.

FT DOMAIN 1721 1810 FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN 2).
 FT DOMAIN 1811 1902 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1903 1991 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 1992 2081 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2082 2201 CONNECTING STRAND 3 (CS-3) (V REGION).
 FT DOMAIN 2202 2283 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2284 2338 FIBRONECTIN TYPE-I 10.
 FT DOMAIN 2339 2381 FIBRONECTIN TYPE-I 11.
 FT DOMAIN 2382 2426 FIBRONECTIN TYPE-I 12.
 FT SITE 1614 1616 CELL ATTACHMENT SITE.
 FT SITE 2181 2183 CELL ATTACHMENT SITE.
 FT DISULFID 53 79 BY SIMILARITY.
 FT DISULFID 77 88 BY SIMILARITY.
 FT DISULFID 98 126 BY SIMILARITY.
 FT DISULFID 124 136 BY SIMILARITY.
 FT DISULFID 142 170 BY SIMILARITY.
 FT DISULFID 168 180 BY SIMILARITY.
 FT DISULFID 187 216 BY SIMILARITY.
 FT DISULFID 214 226 BY SIMILARITY.
 FT DISULFID 232 261 BY SIMILARITY.
 FT DISULFID 259 271 BY SIMILARITY.
 FT DISULFID 308 335 BY SIMILARITY.
 FT DISULFID 333 342 BY SIMILARITY.
 FT DISULFID 360 386 BY SIMILARITY.
 FT DISULFID 374 401 BY SIMILARITY.
 FT DISULFID 420 446 BY SIMILARITY.
 FT DISULFID 434 461 BY SIMILARITY.
 FT DISULFID 470 498 BY SIMILARITY.
 FT DISULFID 496 508 BY SIMILARITY.
 FT DISULFID 518 545 BY SIMILARITY.
 FT DISULFID 543 555 BY SIMILARITY.
 FT DISULFID 561 589 BY SIMILARITY.
 FT DISULFID 587 599 BY SIMILARITY.
 FT DISULFID 2296 2325 BY SIMILARITY.
 FT DISULFID 2323 2335 BY SIMILARITY.
 FT DISULFID 2341 2368 BY SIMILARITY.
 FT DISULFID 2366 2378 BY SIMILARITY.
 FT DISULFID 2385 2409 BY SIMILARITY.
 FT DISULFID 2407 2423 BY SIMILARITY.
 FT DISULFID 2458 2458 INTERCHAIN (WITH 2458 OF OTHER CHAIN).
 FT DISULFID 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN).
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1290 1290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2198 2198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPLIC 1720 1809 Missing (in isoform 2).
 FT VARSPLIC 2082 2106 /FTID=VSP_003258.
 FT VARSPLIC 2082 2200 Missing (in isoform 3).
 FT VARSPLIC 2082 2200 /FTID=VSP_003259.
 FT VARSPLIC 2082 2200 Missing (in isoform 4).
 FT CONFLICT 2318 2318 /FTID=VSP_003260.
 FT SEQUENCE 2477 AA; 272510 MM; B4391A47ECDEB5 CRC64;
 SQ
 Query Match 93.8%; Score 1877; DB 1; Length 2477.
 Best Local Similarity 93.2%; Pred. No. 3.7e-147; Indels 0; Gaps 0;
 Matches 316; Conservative 13; Mismatches 10;
 QY 3 AVYQPPHPQPPYGHCVTDGVSVMQMLTKGNKQMLCTCLANGVSCQETAVTQY 62
 DB 292 AIVQPTHPQPAHYGHCVTDGVSVMQMLTKSQDKQMLCTCLANGVSCQETAVTQY 351
 QY 63 GGSNSNEPCVLPFTYNGRTFTYCTTEGRDGHLMCSTSYBEDQKXSFCTDITVYQTR 122
 DB 352 GGSNSNEPCVLPFTYNGRTFTYCTTEGRDGHLMCSTSYBEDQKXSFCTDITVYQTR 411
 QY 123 GGSNGALGHFPLVNNHYVTDCTSEGRDMMKCGTTONYDADQKFGCPMAAHEICT 182

Db 412 GGNNGALCHPEFLYXSNBNYSDCTSEGRDMMKCGTTQNTDADOKGFGFCMAAHEICT 471
Qy 183 TNEGVWRIQDQMDQKDHMGHMRCTCVNGRGWTCIAYSQLRDOCIYDDITVNVNDF 242
Db 472 TNEGVWRIQDQMDQKDHMGHMRCTCVNGRGWTCIAYSQLRDOCIYDDITVNVNDF 531
Qy 243 HKRHEEGHMLNCTGCGGCGRWKCDPVUDCCDSEFTGTYYQIGDSMEKXVHGVRRQCYG 302
Db 532 HKRHEEGHMLNCTGCGGCGRWKCDPIDRCDDSEFTGTYYQIGDSMEKXVHGVRRQCYG 591
Qy 303 RGIGEMHCQPLQTPSSSGPVEFTFTEPSPQNSHPQM 341
Db 592 RGIGEMHCQPLQTPGTTGPVQVITTEPSPQNSHPQM 630

RESULT 4
FINC_XENLA STANDARD; PRT; 2481 AA.
ID_FINC_XENLA
AC Q91740;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinectin precursor.
GN FN1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9211942; PubMed=1730390;
RA Desimone D.W., Norton P.A., Hynes R.O.;
RT "Identification and characterization of alternatively spliced
RT fibrinectin mRNAs expressed in early Xenopus embryos.";
RL Dev. Biol. 149:357-369(1992).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).
CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC domain-A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibrinectin and absent in others;
CC Name=1;
CC IsoId=Q91740-1; Sequence=Displayed; EMBRYO, CELLULAR FORMS OF
CC -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
CC FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAIN. IN
CC FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
CC CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC -1- SIMILARITY: Contains 12 fibrinectin type I domains.
CC -1- SIMILARITY: Contains 2 fibrinectin type II domains.
CC -1- SIMILARITY: Contains 17 fibrinectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M77820; AAA49707.1; -
DR HSSP; P02751; 2FN2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; Fn1; 12.

DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Alternative splicing; Signal.
FT SIGNAL 1 31
FT CHAIN 32 2481
FT DOMAIN 55 275
FT DOMAIN 309 609
FT DNA_BIND 907 1172
FT DOMAIN 1358 1631
FT DOMAIN 1812 2082
FT DOMAIN 2301 2432
FT DOMAIN 53 93
FT DOMAIN 187 231
FT DOMAIN 232 276
FT DOMAIN 307 346
FT DOMAIN 346 405
FT DOMAIN 406 470
FT DOMAIN 469 512
FT DOMAIN 517 559
FT DOMAIN 560 603
FT DOMAIN 610 707
FT DOMAIN 708 809
FT DOMAIN 810 904
FT DOMAIN 905 995
FT DOMAIN 996 1085
FT DOMAIN 1086 1173
FT DOMAIN 1174 1265
FT DOMAIN 1266 1356
FT DOMAIN 1357 1447
FT DOMAIN 1448 1537
FT DOMAIN 1538 1631
FT DOMAIN 1632 1721
FT DOMAIN 1722 1811
FT DOMAIN 1812 1903
FT DOMAIN 1904 1992
FT DOMAIN 1993 2082
FT DOMAIN 2083 2205
FT DOMAIN 2206 2287
FT DOMAIN 2289 2343
FT DOMAIN 2344 2386
FT DOMAIN 2388 2431
FT SITE 1615 1617
FT DISULFID 55 81
FT DISULFID 79 90
FT DISULFID 100 128
FT DISULFID 126 138
FT DISULFID 144 172
FT DISULFID 170 182
FT DISULFID 189 218
FT DISULFID 216 228
FT DISULFID 234 263
FT DISULFID 261 273
FT DISULFID 291 309
FT DISULFID 309 336
FT DISULFID 334 343
FT DISULFID 361 387
FT DISULFID 375 402
FT DISULFID 421 447
FT DISULFID 447 499
FT DISULFID 497 509
FT DISULFID 519 546
FT DISULFID 544 556
FT DISULFID 562 590
FT DISULFID 588 600
FT FIBRONECTIN.
FT FIBRIN- AND HEPARIN-BINDING 1.
FT COLLAGEN-BINDING.
FT BY SIMILARITY.
FT CELL-ATTACHMENT.
FT HEPARIN-BINDING 2.
FT FIBRIN-BINDING 2.
FT FIBRONECTIN TYPE-1 1.
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FT FIBRONECTIN TYPE-1

FT DISULFID 2301 2330 BY SIMILARITY.
 FT DISULFID 2328 2340 BY SIMILARITY.
 FT DISULFID 2346 2373 BY SIMILARITY.
 FT DISULFID 2371 2383 BY SIMILARITY.
 FT DISULFID 2390 2414 BY SIMILARITY.
 FT DISULFID 2412 2428 BY SIMILARITY.
 FT DISULFID 2459 2459 INTERCHAIN (WITH 2463 OF OTHER CHAIN)
 FT DISULFID 2463 2463 (BY SIMILARITY).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1244 1244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1291 1291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2202 2202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2481 AA; 272678 MW; 7E47DF4F6CE72C93 CRC64;

Query Match 79.5%; Score 1591; DB 1; Length 2481;
 Best Local Similarity 77.6%; Pred. No. 1,6e-123;
 Matches 263; Conservative 41; Mismatches 33; Indels 2; Gaps 1;

QY 3 AVYQPPHPQPPYHGVTVDSGVVYVGMQLTQGNKQMLCTCLANGVSCQETAVTQTY 62
 DB 295 ALVQPD--SGLBPGHCVTDNGVLVSLGMKRWLTQSGKQMLCTCLANGVSCQETAVTIF 352
 QY 63 GGNNSNEPCVLPFTYNGRTYSCCTBGRONGHLMCTSTSYEDQKTSFCTDITVLYQTR 122
 DB 353 GGNANBEPKAIPTTHQKTYSCCTBGRONGHLMCTSTSYEDQKTSFCTDITVLYQTR 412
 QY 123 GGNNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNYADQKFGCPMAHEICT 182
 DB 413 GGNNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNYADQKFGCPMAHEICT 472
 QY 183 TNEGVRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQLRDQCIYDITVYVNDIF 242
 DB 473 TNEGVRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQLRDQCIYDITVYVNDIF 532
 QY 243 HKHBEHMLNCTCFQGRGRMKCDPVDQCDSETGTFTYIGSWKXVHGVYQCYG 302
 DB 533 TKLBEHMLNCTCFQGRGRMKCDPVDQCDSETGTFTYIGSWKXVHGVYQCYG 592
 QY 303 RGIGEMHCOPLQTPSSGPEVETITETPSQPSHPLOW 341
 DB 593 RGIGEMHCOPLQTPSSGPEVETITETPSQPSHPLOW 631

RESULT 5

FINC NOTVI STANDARD; PRT; 190 AA.

AC Q91400;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Fibronectin (Fragment).
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Notoptthalmus.
 NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95252528; PubMed=7734733;
 RA Nace J.D., Tassava R.A.;
 RT Examination of fibronectin distribution and its sources in the
 RT regenerating newt limb by immunocytochemistry and in situ
 RT hybridization.
 RL Dev. Dyn. 202;153-164(1995).
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).

CC -1- FUNCTION: BENEATH WOUND EPITHELIUM, FIBRONECTIN PROBABLY PROVIDES
 CC A SUBSTRATE ON WHICH THE DIFFERENTIATION STUMP TISSUE CELLS WILL
 CC MIGRATE AND ACCUMULATE.
 CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
 CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
 CC -1- SIMILARITY: Contains at least 1 fibronectin type II domain.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL/ S76886; AAB34250.1; -
 DR PIR; I51279; I51279.
 DR HSP; P02751; 2FN2.
 DR InterPro; IPR000083; Fibronctn1.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00039; Fn1; 3.
 DR Pfam; PF00040; Fn2; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR ProDom; PD000995; FN_Type_II; 1.
 DR SMART; SM00058; FN1; 3.
 DR SMART; SM00059; FN2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 KW Repeat.
 FT FT NON TER 1 1
 FT DOMAIN <1 56
 FT DOMAIN 55 98
 FT DOMAIN 103 145
 FT DOMAIN 146 >190
 FT DISULFID 57 85
 FT DISULFID 83 95
 FT DISULFID 105 132
 FT DISULFID 130 142
 FT CARBOHYD 17 17
 FT CARBOHYD 115 115
 FT CARBOHYD 129 129
 FT NON TER 190 190
 SQ SEQUENCE 190 AA; 21960 MW; 2C2033226DB4233 CRC64;

Query Match 48.0%; Score 961; DB 1; Length 190;
 Best Local Similarity 85.8%; Pred. No. 1,1e-72;
 Matches 163; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 125 NSNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNYADQKFGCPMAHEICTTN 184
 DB 1 NSNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNYADQKFGCPMAHEICTTN 60
 QY 185 EGVMYRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQLRDQCIYDITVYVNDIF 244
 DB 61 EGVMYRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQLRDQCIYDITVYVNDIF 120
 QY 245 RHEBGMNCTCFQGRGRMKCDPVDQCDSETGTFTYIGSWKXVHGVYQCYG 304
 DB 121 RHEBGMNCTCFQGRGRMKCDPVDQCDSETGTFTYIGSWKXVHGVYQCYG 180
 QY 305 IGEWHCOPLQ 314
 DB 181 IGEWHCOPLQ 190

RESULT 6

MM09_RABIT STANDARD; PRT; 707 AA.

ID MM09_RABIT
 AC P41246;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN MMP9.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Bone;
 RX MEDLINE=94253056; PubMed=8195136;
 RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
 RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
 RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts";
 RL J. Biol. Chem. 269:15006-15009 (1994).
 RN [2]
 RP SEQUENCE OF 1-171 FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RX MEDLINE=95050662; PubMed=7961810;
 RA Fitt M.E., Bartlett J.D., Matsubara M., Rinehart W.B., Mody M.K.,
 RA Girard M.T., Rainville M.;
 RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of API and
 AP2 in cell type-specific transcription.";
 RL J. Biol. Chem. 269:28620-28628 (1994).
 CC -1 FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1 CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1 COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1 TISSUE SPECIFICITY: OSTEOCLASTS.
 CC -1 SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1 SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1 SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D26514; BAA05520.1; -;
 DR EMBL: L36050; AAA64358.1; -;
 DR PIR: A53796; A53796.
 DR HSSP: P08254; 1COR.
 DR MEROPS: M10_004; -;
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Matrxin.
 DR InterPro: IPR006026; Nzn_Mtpeptidase.
 DR InterPro: IPR006970; PT.
 DR InterPro: IPR006025; Zn_Mtpeptidase.
 DR Pfam: PF00040; fn2; 3.
 DR Pfam: PF00045; hemopexin; 4.
 DR Pfam: PF00413; peptidase_M10; 1.
 DR Pfam: PF03933; peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS: PRO0013; FNTYPEII.
 DR PRINTS: PRO0138; MATRXIN.
 DR PRODOM: PD000995; FN_Type_II; 3.
 DR SMART: SM00059; FN2; 3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZNMC; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 KW Hydrolase; Metalloproteinase; Glycoprotein; Zinc; Zymogen; Calcium;

KW Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL 1
 FT PROPEP 20
 FT CHAIN 107
 FT DOMAIN 107
 FT DOMAIN 223
 FT DOMAIN 281
 FT DOMAIN 340
 FT DOMAIN 397
 FT SITE 513
 FT SITE 99
 FT METAL 401
 FT ACT SITE 402
 FT METAL 405
 FT METAL 411
 FT CARBOHYD 88
 FT CARBOHYD 120
 FT CARBOHYD 127
 FT DISULFID 516
 FT CONFLICT 76
 FT CONFLICT 100
 SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;
 Query Match 19.8%; Score 396.5; DB 1; Length 707;
 Best Local Similarity 45.4%; Pred. No. 2.2e-25;
 Matches 79; Conservative 23; Mismatches 49; Indels 23; Gaps 6;
 QY 16 YGHCVTDSGVVSYVMQMLKTQGNKQMLCTCLGNGVSCQETAVLYQYGGNSGEPVLPF 75
 DB 241 YTACTTGG--RSDGMAMCSTTADYD--TDRRGFGPSESLYIQ--DGNADGKPCPEPF 292
 QY 76 TYNRTYSCCTBEROGHLMCTSTSYEDQKSF--TDHIVLYVOTRGNSNGALCH 132
 DB 293 IFQRTYSACTDGRSDGHRWCATYADKDLGFCPTRADSTIV--GNSAGEICLV 348
 QY 133 PPFLLYNNHNTDCTSEGRPRDMKWCCTONYVDADQKGFPC-----MAHE 178
 DB 349 PPFVFLGKRYISCTSEGRDRGLWCATITSNFSDKMKWFCPEDKYSFLVAHE 402
 RESULT 7
 MM02_RABIT STANDARD; PRT; 662 AA.
 AC P50757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
 GN MMP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Articular joint;
 RX MEDLINE=96283805; PubMed=8679695;
 RA Matsunoto S., Katoh M., Matanabe T., Masuh Y.;
 RT "Molecular cloning of rabbit matrix metalloproteinase-2 and its broad
 RT expression at several tissues";
 RL Biochim. Biophys. Acta 1307:137-139 (1996).
 CC -1 CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-gln-gly-|-
 CC Ile-Ala-gly-Gln.
 CC -1 COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1 SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1 PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3) (By similarity).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1 SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1 SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
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DR EMBL; D63579; BAA09796.1; -
 DR PIR; S70365; S70365.
 DR HSSP; P08253; 1RTG.
 DR MEROPS; M10.003; -
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL; 1 29
 FT PROPEP 30 109
 FT CHAIN 110 662
 FT DOMAIN 110 221
 FT DOMAIN 222 396
 FT DOMAIN 397 467
 FT DOMAIN 226 283
 FT DOMAIN 284 341
 FT DOMAIN 342 399
 FT DOMAIN 399 468
 FT SITE 102 102
 FT METAL 403 403
 FT METAL 404 404
 FT ACT SITE 407 407
 FT METAL 413 413
 FT CARBOHYD 575 575
 FT CARBOHYD 644 644
 FT DISULFID 471 662
 FT SEQUENCE 662 AA; 73803 MW; 1CC246B270E440C8 CRC64;

Query Match 19.3%; Score 386.5; DB 1; Length 662;
 Best Local Similarity 38.8%; Pred. No. 1.4e-24;
 Matches 80; Conservative 29; Mismatches 76; Indels 21; Gaps 6;

QY 55 ETAVTQYGGNSNEPCVLPVTNGRTFYSGTTEGRDDHLMCTSTNYEQDQKXSTCTD 114
 DB 217 EGVVRYKYNADEYCKFPFLFGKEYTSTCTDGRSDGFLWCSTYTNFEDDGYGFC-P 275
 QY 115 HTVLVVRGNSNGLCHPFLVYNNHYTDCSTSEGRDNMKMCTTQNYADQKFGFCPM 174
 DB 276 HEALF-TMGSNADQCPKCFPRFGTSTYSGTTEGRDGRKWCCTTDYDRDKYGGFCPE 334
 QY 175 AAHEICTTNEG- - - - -MYRIGQMDKQHDHMMKCTCVNGRGEMTCTA- - - - -YSQLR 226
 DB 335 TANGSTIGNSGACVCFPFPLFGKYES- - - - -CTSAGRSDGKMWCTSTNYDDDR 385
 QY 227 DQCTVDDITVNVNTFFKHEEGHML 252
 DB 386 KWGFCPDQGYSL-FLVAHAEFGHAM 409

RESULT 8

MM02_MOUSE
 ID MM02_MOUSE STANDARD; PRT; 662 AA.
 AC P3434;
 DT 01-FBB-1994 (Rel. 28, Created)
 DT 01-FBB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
 GN MMP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2218452; PubMed=1373140;
 RA Reponen P., Sahberg C., Huhtala P., Hurskainen T., Thesleff I.,
 RA Tytgavaen K.;
 RT "Molecular cloning of murine 72-kDa type IV collagenase and its
 RT expression during mouse development."
 RL J. Biol. Chem. 267:7856-7862(1992).
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-[
 CC Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3) (by similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC or send an email to license@sb-sib.ch).

DR EMBL; M84324; AAA39338.1; -
 DR PIR; A42496; A42496.
 DR HSSP; P08253; 1RTG.
 DR MEROPS; M10.003; -
 DR MGD; MGI:97009; MMP2.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL; 1 29
 FT PROPEP 30 109
 FT CHAIN 110 662
 FT DOMAIN 110 221
 FT DOMAIN 222 396
 FT DOMAIN 397 467
 FT DOMAIN 226 283

DB 335 TAWSTVGNSEGAFCVPPFTFLNKKYES-----CTSGNRDCKWCATTTNVDDB 385
 QY 227 DQCIYDITVNVNDTFHKEBGM 252
 DB 386 KMGFCPDGYSTL--FLVAHEFGHAM 409

RESULT 10
 ID_MM02_HUMAN STANDARD; PRT; 660 AA.
 AC P08253;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A)
 DE (TBE-1).
 GN MMP2 OR CLG4A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 19-660 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88198218; PubMed=2834383;
 RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
 RA Selster J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.,
 RT "H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
 RT secrete a single metalloproteinase capable of degrading basement
 RT membrane collagen".
 RL J. Biol. Chem. 263:6579-6587(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91236162; PubMed=1851724;
 RA Collier I.E., Burns G.A.P., Goldberg G.I., Gerhard D.S.,
 RT "On the structure and chromosome location of the 72- and 92-kDa human
 RT type IV collagenase genes".
 RL Genomics 9:429-434(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90293047; PubMed=2162831;
 RA Huhtala P., Chow L.T., Trygvaason K.,
 RT "Structure of the human type IV collagenase gene".
 RL J. Biol. Chem. 265:11077-11082(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marzula K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uding T.B., Toibiyuki S., Cannici P., Prange C.,
 RA Raha S.S., Loughelino N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smallin D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE=90228972; PubMed=2158484;
 RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.,
 RA Trygvaason K.,

RT "Completion of the primary structure of the human type IV collagenase
 RT preproenzyme and assignment of the gene (CLG4) to the q21 region of
 RT chromosome 16".
 RL Genomics 6:554-559(1990).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
 RX MEDLINE=96069777; PubMed=758364;
 RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
 RA Lattman E.E.,
 RT "Crystal structure of the haemopexin-like C-terminal domain of
 RT gelatinase A".
 RL Nat. Struct. Biol. 2:938-942(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.
 RX MEDLINE=96140723; PubMed=8549817;
 RA Golike U., Gomis-Ruth F.X., Crabbe T., Murphy G., Docherty A.J.,
 RA Bode W.,
 RT "The C-terminal (haemopexin-like) domain structure of human
 RT gelatinase A (MMP2): structural implications for its function".
 RL FEBS Lett. 378:126-130(1996).
 CC -1- CATALYTIC ACTIVITY: cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
 CC Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC -----
 DR EMBL: J03210; AAA5701.1; -
 DR EMBL: M33789; AAA52027.1; -
 DR EMBL: M55593; AAA52028.1; -
 DR EMBL: M55593; AAA52028.1; JOINED.
 DR EMBL: M55582; AAA52028.1; JOINED.
 DR EMBL: M55583; AAA52028.1; JOINED.
 DR EMBL: M55584; AAA52028.1; JOINED.
 DR EMBL: M55585; AAA52028.1; JOINED.
 DR EMBL: M55586; AAA52028.1; JOINED.
 DR EMBL: M55587; AAA52028.1; JOINED.
 DR EMBL: M55588; AAA52028.1; JOINED.
 DR EMBL: M55589; AAA52028.1; JOINED.
 DR EMBL: M55590; AAA52028.1; JOINED.
 DR EMBL: M55591; AAA52028.1; JOINED.
 DR EMBL: M55592; AAA52028.1; JOINED.
 DR EMBL: BC002576; AAH02576.1; -
 DR EMBL: A28153; A28153.
 DR PDB: 1RTG; 10-JUN-96.
 DR PDB: 1GEN; 17-AUG-96.
 DR PDB: 1CK7; 25-AUG-99.
 DR PDB: 1CKW; 12-NOV-99.
 DR PDB: 1HOV; 20-DEC-02.
 DR PDB: 1U7M; 22-AUG-01.
 DR PDB: 1KSO; 17-APR-02.
 DR PDB: 1QIB; 19-NOV-99.
 DR MEROPS: M10.003; -.
 DR Genew: HGNC:7166; MMP2.
 DR MIM: 120360; -
 DR GO: GO:000615; Extracellular space; TAS.
 DR GO: GO:000428; F:gelatinase A activity; TAS.
 DR GO: GO:0008270; F:zinc ion binding activity; TAS.
 DR InterPro: IPR000562; FN Type II.
 DR InterPro: IPR000585; Hemopexin.

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DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Zn_MTPeptide.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; peptidase_M10; 1.
DR PRINTS; PR00013; ENTPEP1.
DR PRINTS; PR00138; MATRILIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; Zmnc; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 109 ACTIVATION PEPTIDE.
FT CHAIN 110 660 72 kDa type IV COLLAGENASE.
FT DOMAIN 110 221 COLLAGENASE-LIKE 1.
FT DOMAIN 222 396 COLLAGEN-BINDING.
FT DOMAIN 397 465 COLLAGENASE-LIKE 2.
FT DOMAIN 226 283 FIBRONECTIN TYPE-II 1.
FT DOMAIN 342 399 FIBRONECTIN TYPE-II 2.
FT DOMAIN 466 660 FIBRONECTIN TYPE-II 3.
FT SITE 102 102 HEMOPEXIN-LIKE.
FT METAL 403 403 CYSTEINE SWITCH (POTENTIAL).
FT ACT_SITE 404 404 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 407 407 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 413 413 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 468 660
FT TURN 468 470
FT STRAND 477 481
FT TURN 482 483
FT STRAND 484 489
FT TURN 490 491
FT STRAND 492 496
FT TURN 499 500
FT STRAND 504 508
FT HELIX 509 511
FT TURN 512 512
FT TURN 514 515
FT STRAND 522 526
FT TURN 527 530
FT STRAND 531 536
FT TURN 537 538
FT STRAND 539 544
FT TURN 545 546
FT STRAND 547 548
FT TURN 550 551
FT STRAND 554 555
FT HELIX 556 559
FT TURN 560 560
FT TURN 563 564
FT TURN 570 574
FT STRAND 575 578

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Query Match 19.1%; Score 382.5; DB 1; Length 660;
 Best Local Similarity 38.3%; Pred. No. 2.9e-24;
 Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

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QY 55 ETAVTQTGYGNSNBPCLPTFYNGRTFYSCTEGRQGHLMCTSTSYEDOKYSPCTD 114
Db 217 EGVGVRYKYGNADEYCKFPFLFNCKEYNSCTDGRSGFLMCSCTTYFEKDGKYGFC-P 275
QY 115 HTVLVQTRGNSNGALCHFPFLYNNHNYTDCTSGGRDNMKWCGTTONYDADOKFGFCPM 174

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Db 276 HEALF-TWGNVAEQPKFPFRFGTSTYDSCTTTEGRDGYRWCGITBDYDRKRYGFCPE 334
QY 175 AAHEICTNMGV-----MVRIGQMDKQHDMMAMRCTGVNGRGWTGCA---YSGLR 226
Db 335 TAMSTVGNSESGACVCFPTFLGNKYES-----CTSGRSDGKMKWCAITANYDDDR 385
QY 227 DQCIYDDITVNVNDTFKRHEGHML 252
Db 386 KWGFCPDGYSL--FLVAHEFGHAM 409

RESULT 11
ID MM02 CHICK STANDARD; PRT; 663 AA.
AC 090611;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN MMP2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94280397; PubMed=8010954;
RA Aimes R.T., French D.L., Quigley J.P.;
RT "Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from
RT chicken embryo fibroblasts using gene family PCR: expression of the
RT gelatinase increases upon malignant transformation."
RL Biochem. J. 300:729-736 (1994).
RN [2]
RP SEQUENCE OF 27-41 AND 107-122.
RX MEDLINE=91161603; PubMed=1848240;
RA Chen J.-M., Aimes R.T., Ward G.R., Youngleib G.L., Quigley J.P.;
RT "Isolation and characterization of a 70-kDa metalloproteinase
RT (gelatinase) that is elevated in Rous sarcoma virus-transformed
RT chicken embryo fibroblasts."
RL J. Biol. Chem. 266:5113-5121 (1991).
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-Ile-
CC Ile-Ala-Gly-Gln.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
CC -1- PM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
CC MMP3) (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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CC -----
DR EMBL; U07775; AAA19596.1; -.
DR PIR; S46492; S46492.
DR HSSP; P08253; IRTG.
DR MEROPS; M10.003; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Zn_MTPeptide.
DR InterPro; IPR006025; Zn_MTPeptide.

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DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; ENTPEPIT.
 DR PRINTS; PR00138; MATRXIN.
 DR Prodom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZMNC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR Hydroxylase; Metalloprotease; Zinc; Zymogen; Calcium; Repeat;
 KM Collagen degradation; Extracellular matrix; Signal.
 FT SIGNAL 1 26
 FT PROPEP 27 106 ACTIVATION PEPTIDE.
 FT CHAIN 107 663 72 kDa type IV COLLAGENASE.
 FT DOMAIN 107 218 COLLAGENASE-LIKE 1.
 FT DOMAIN 219 393 COLLAGEN-BINDING.
 FT DOMAIN 394 468 COLLAGENASE-LIKE 2.
 FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 281 338 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 339 396 FIBRONECTIN TYPE-II 3.
 FT DOMAIN 469 663 HEMOPEXIN-LIKE.
 FT SITE 99 99 CYSTEINE SWITCH (POTENTIAL).
 FT METAL 400 400 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 401 401 BY SIMILARITY.
 FT METAL 404 404 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 410 410 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISUFID 472 663 BY SIMILARITY.
 FT CONFLICT 40 40 P -> Q (IN REF. 2).
 FT CONFLICT 116 116 W -> T (IN REF. 2).
 FT CONFLICT 122 122 T -> I (IN REF. 2).
 SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA867C3EBCA CRC64;

Query Match 19.1%; Score 382.5; DB 1; Length 663;
 Best Local Similarity 37.0%; Pred. No. 2.9e-24;

Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;

QY 55 ETAVTQYGGNSGECVLPFTYNGRTFYSCTEGRDGHLMGCTTSNYEQDKYSFCTD 114
 Db 214 EGVVAVKYGMAAGEYCKPFPMNGKYNKCTDAGRNDGLMCTTDPPADKYGCPH 273
 QY 115 HTLVVOTRGNSNGALCHPEPLNNHNYTDCISEGRDNNKMKCTTQNYADQKFGFCPM 174
 Db 274 ESIF--TMGNGDGOECKPFPEKFGQSYDQCTTEGRDGYRWCCTEDYDRDKYGFCE 331
 QY 175 AAHEBICITNEGIV-----WRIQDQMKQHDNMGHMRCTGVNGRGRTGIAVSQLRDQ- 228
 Db 332 TANSTVGNSGEGAPCVPFPIFLNKKYDS-----CTAGRNNDGLMCASTSSYDDDR 382
 QY 229 ----CIVDITVNVNDTFHRRHEEGHML 252
 Db 383 KMGFC--PDGYSL--FLVAHHRFGHAM 406
 RESULT 12
 MM09 RAT STANDARD; PRT; 708 AA.
 AC PS0282;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN MMP9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer 344;
 RX MEDLINE=96184505; PubMed=8605986;
 RA Xia Y., Garcia G., Chen S., Wilson C.B., Feng L.;
 RT "Cloning of rat 92-kDa type IV collagenase and expression of an
 RT active recombinant catalytic domain";
 RL FEBS Lett. 382:285-288 (1996).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M1star;
 RX MEDLINE=96069602; PubMed=7590350;
 RA Okada A., Santavica M., Bassett P.;
 RT "The cdna cloning and expression of the gene encoding rat gelatinase
 RT B";
 RL Gene 164:317-321 (1995).
 CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COPACITOR: Binds 2 zinc ions per subunit, calcium (by similarity).
 CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC -----
 DR EMBL; U36476; AA01721.1; -;
 DR EMBL; U24441; AA090911.1; -;
 DR PIR; JCA364; JCA364.
 DR PIR; S62907; S62907.
 DR HSSP; P08254; IUSN.
 DR MEROPS; M10.04; -;
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR006026; NZn_MTPeptide.
 DR InterPro; IPR006970; PT.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF03933; Peptidase_M10; 1.
 DR Pfam; PF04886; PT; 1.
 DR PRINTS; PR00013; ENTPEPIT.
 DR PRINTS; PR00138; MATRXIN.
 DR Prodom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZMNC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 KW Hydroxylase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KW Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 107 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 108 708 92 kDa type IV COLLAGENASE.
 FT DOMAIN 224 281 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 282 340 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 341 398 FIBRONECTIN TYPE-II 3.
 FT DOMAIN 516 708 HEMOPEXIN-LIKE.
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 FT METAL 402 402 ZINC (CATALYTIC) (BY SIMILARITY).

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FT ACT_SITE 403 403 BY SIMILARITY.
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FT METAL 412 412 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CONFLICT 2 2 S -> N (IN REF. 2).
FT CONFLICT 112 112 D -> E (IN REF. 2).
FT CONFLICT 326 327 AD -> LY (IN REF. 2).
FT CONFLICT 364 364 S -> G (IN REF. 2).
FT CONFLICT 441 441 H -> Q (IN REF. 2).
FT CONFLICT 472 472 S -> P (IN REF. 2).
FT CONFLICT 515 515 D -> V (IN REF. 2).
FT CONFLICT 551 551 N -> S (IN REF. 2).
FT CONFLICT 566 566 F -> L (IN REF. 2).
FT CONFLICT 568 568 S -> A (IN REF. 2).
FT CONFLICT 579 579 P -> S (IN REF. 2).
FT CONFLICT 589 589 LMAQ -> SGRK (IN REF. 2).
FT CONFLICT 597 597 S -> T (IN REF. 2).
FT CONFLICT 669 669 Q -> H (IN REF. 2).
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QY 47 LGNGVSCQETAVTGTGGNSNGEPCVLPFTNGRTFVSCTEGRDGHLMCSTTSNEYOD 106
DB 213 LGKG-----AVPEFTFGNANGACHPEFTFGRSYSTCTTDGNDGKPMGCTTADYD 266
QY 107 QKISFCTDHTVLVOTRGNSNGALCHPEFTLYNNHNYDCTSEGRDNMKWCGTTONYAD 166
DB 267 RKYFPCSEEN--LYTEHGNGDGKPCVFPFIEGHSHYSACTKGRSDGYRCATTANYDQD 324
QY 167 QKQEGCMAAHEELCTTNE--GVN-----YRIGDQMDKHMDGHMRCCTCVNGGERTCI 220
DB 325 KADGECPRADVTYTGNSAEMCVFPFVFGKQYS-----TCTSEGRSDGRMCA 375
QY 221 AYSQI--RDQCIYDITVYNTDTPFKHREGHML 252
DB 376 TTSTNFDADKKWGFCEPDGYSI--FLVVAHREGHML 408

RESULT 13
MM09 MOUSE STANDARD: PRT; 730 AA.
ID MM09 MOUSE STANDARD: PRT; 730 AA.
AC P41245; 006788; O9DC02;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
CN MMP9 OR CLG4B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
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RC TISSUE=Bone;
RX MEDLINE=94179406; PubMed=8132709;
RA Reponen P., Sahberg C., Munaut C., Theleff I., Trygvaason K.;
RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
RT osteoclast lineage during mouse development.";
RL J. Cell Biol. 124:1091-1102(1994).
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RP SEQUENCE FROM N.A.
RX MEDLINE=93176173; PubMed=8382489;
RA Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 190:732-740(1993).

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RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=94062823; PubMed=8243459;
RA Masure S., Nys G., Fiten P., van Damme J., Odenakker G.;
RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
RT glycosylation in WEHI-3 macrophages and gene organisation.";
RL Eur. J. Biochem. 218:129-141(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94033534; PubMed=8219207;
RA Grubert T., Johnston J., Berliner N.;
RT "Cloning and expression of the cDNA encoding mouse neutrophil
RT gelatinase: demonstration of coordinate secondary granule protein
RT gene expression during terminal neutrophil maturation.";
RL Blood 82:3192-3197(1993).
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohenki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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 DR Pfam: PF00045; hemopexin; 4.
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 DR Pfam: PF03933; peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 2.
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 DR PRINTS: PR00138; MATRILIN.
 DR PRODOM: PD000995; FN_Type_II; 3.
 DR SMART: SM00059; FN2; 3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZnMC; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00023; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
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 FT DOMAIN 531 730 HEMOPEXIN-LIKE.
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 FT ACT SITE 402 402 BY SIMILARITY.
 FT METAL 405 405 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 411 411 ZINC (CATALYTIC) (BY SIMILARITY).
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 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT VARIANT 711 711 P -> H.
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 FT CONFLICT 25 26 QP -> HA (IN REF. 4).
 FT CONFLICT 466 466 P -> T (IN REF. 5).
 FT CONFLICT 514 514 A -> P (IN REF. 5).
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 FT CONFLICT 711 711 P -> H (IN REF. 5).
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 Matches 79; Conservative 26; Mismatches 52; Indels 40; Gaps 8;

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RESULT 14
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 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B
 DE (GELB).
 GN MMP9.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
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 RX MEDLINE=95287902; PubMed=7770085;
 RA Baylis H.A., Megson A., Hall R.;
 RT "infection with Theileria annulata induces expression of matrix
 RT metalloproteinase 9 and transcription factor AP-1 in bovine
 RT leucocytes.";
 RL Mol. Biochem. Parasitol. 69:211-222(1995).
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 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
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 DR HSSP; P22894; IJAP.
 DR MEROPS: M10.004; -.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Matrilin.
 DR InterPro: IPR006026; Nzn_MTPeptidase.
 DR InterPro: IPR006970; PT.
 DR InterPro: IPR006025; Zn_MTPeptidase.
 DR Pfam: PF00040; fn2_3.
 DR Pfam: PF00045; hemopexin; 4.
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 DR Pfam: PF03933; peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
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 DR PRINTS: PR00138; MATRILIN.
 DR PRODOM: PD000995; FN_Type_II; 3.
 DR SMART: SM00059; FN2; 3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZnMC; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00023; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT PROPEP 20 106 ACTIVATION PEPTIDE.
 FT CHAIN 107 712 92 kDa TYPE IV COLLAGENASE.
 FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 281 339 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 340 397 FIBRONECTIN TYPE-II 3.
 FT DOMAIN 518 712 HEMOPEXIN-LIKE.

FT SITE 99 99 CYSTEINE SWITCH (BY SIMILARITY).
 FT METAL 401 401 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 402 402 BY SIMILARITY.
 FT METAL 405 405 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 411 411 ZINC (CATALYTIC) (BY SIMILARITY).
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 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
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 ON NCBI_TaxID=9606;
 RX MEDLINE=90008879; PubMed=251898;
 RA Wilhelm S.M., Collier I.E., Warner B.L., Eisen A.Z., Grant G.A.,
 RA Goldberg G.I.;
 RA "SV40-transformed human lung fibroblasts secrete a 92-kDa type IV
 RT collagenase which is identical to that secreted by normal human
 RT macrophages.";
 RL J. Biol. Chem. 264:17213-17221(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91358433; PubMed=1653238;
 RA Huhata P., Thutilla A., Chow L.T., Lohi J., Keski-Oja J.,
 RA Tryggyrason K.;
 RA "Complete structure of the human gene for 92-kDa type IV collagenase.
 RT Divergent regulation of expression for the 92- and 72-kilodalton
 RT enzyme genes in HT-1080 cells.";
 RL J. Biol. Chem. 266:16485-16490(1991).
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 RX MEDLINE=21638749; PubMed=11780052;
 RA Jones M., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dharm P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslahti M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Traven A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RA "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISUB=B-cell;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarene P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra W.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=93149601; PubMed=8426746;
 RA Sato H., Seki M.;
 RA "Regulatory mechanism of 92 kDa type IV collagenase gene expression
 RT which is associated with invasiveness of tumor cells.";
 RL Oncogene 8:395-405(1993).
 RN [6]
 RP SEQUENCE OF 20-37.
 RX MEDLINE=91355647; PubMed=1653055;
 RA van Ranst M., Norga K., Maure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., van Damme J., Opdenacker G.;
 RA "The cytokine-protease connection: identification of a 96-kD TGF-
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239(1991).
 RN [7]
 RP SEQUENCE OF 28-60.
 RC TISUB=Neutrophils;
 RX MEDLINE=91249834; PubMed=1645657;
 RA Maure S., Proost P., van Damme J., Opdenacker G.;
 RA "Purification and identification of 91-kDa neutrophil gelatinase.
 RT Release by the activating peptide interleukin-8.";
 RL Eur. J. Biochem. 198:391-398(1991).
 RN [8]
 RP CHARACTERIZATION.
 RA Kang K., Lee D.-H.;
 RA "Purification and characterization of human 92-kDa type IV collagenase

RT (gelatinase B).";
 RL Exp. Mol. Med. 28:161-165(1996).
 RN [9]
 RP 3D-STRUCTURE MODELING.
 RA Mallena S.C., Sagatkar R.D.;
 RT "Theoretical model of human type IV collagenase precursor.";
 RL Submitted (APR-2002) to the PDB data bank.
 RN [10]
 RP VARIANTS VAL-20; LYS-82 AND GLN-279.
 RX MEDLINE=20065865; PubMed=10598806;
 RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.;
 RT "Genetic variation at the matrix metalloproteinase-9 locus on
 chromosome 20q12.2-13.1.";
 RL Hum. Genet. 105:418-423(1999).
 CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (by similarity).
 CC -1- SUBUNIT: EXISTS AS MONOMER, DISULFIDE-LINKED HOMODIMER, AND AS A
 CC HETERODIMER WITH A 25 kDa PROTEIN. MACROPHAGES AND TRANSFORMED
 CC CELL LINES PRODUCE ONLY THE MONOMERIC FORM.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL ALVEOLAR MACROPHAGES AND
 CC GRANULOCYTES.
 CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J05070; AAA51539.1; -;
 DR EMBL: D10051; BAA20967.1; -;
 DR EMBL: AL162458; CAC10459.1; -;
 DR EMBL: BC006093; AAH06093.1; -;
 DR PIR: A34458; A34458.
 DR PIR: A34458; A34458.
 DR PDB: 1LKG; 15-MAY-02.
 DR PDB: 1GKC; 16-MAY-02.
 DR PDB: 1GKD; 16-MAY-02.
 DR PDB: 1TV; 04-SEP-02.
 DR MEROPS: M10.004; -;
 DR GlycoSuiteDB: P14780; -;
 DR Genew: HGNC:7176; MMP9.
 DR MIM: 120361; -;
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0008133; F:collagenase activity; TAS.
 DR GO: GO:0008270; F:zinc ion binding activity; TAS.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Matrixin.
 DR InterPro: IPR006026; Nzn_MTPeptidse.
 DR InterPro: IPR006970; PT.
 DR InterPro: IPR006025; Zn_MTPeptidse.
 DR Pfam: PF00040; fn2_3.
 DR Pfam: PF00045; hemopexin; 4.
 DR Pfam: PF00413; Peptidase_M10_1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS: PR00013; FNTYPEII.
 DR PRINTS: PR00138; MATRIXIN.
 DR ProDom: PD000995; FN_Type_II; 3.
 DR SMART: SM00059; FN2_3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZmC; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.

DR PROSITE: PS00024; HEMOPEXIN; 1.
 DR PROSITE: PS00546; CYSTEINE SWITCH; 1.
 KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KW Collagen degradation; Extracellular matrix; Repeat; Signal;
 KW Polymorphism; 3D-structure.
 FT SIGNAL 1 19
 FT PROPEP 20 106
 FT CHAIN 107 707
 FT DOMAIN 223 280
 FT DOMAIN 281 339
 FT DOMAIN 340 397
 FT DOMAIN 513 707
 FT SITE 99 99
 FT METAL 401 401
 FT ACT_SITE 402 402
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 Best Local Similarity 40.1%; Pred. No. 1,6e-23;
 Matches 77; Conservative 29; Mismatches 56; Indels 30; Gaps 7;
 QY 16 YGHCVTDGIVYVSGQWIKTQGNKQMLCTCLGNGVSCQETAVTQYVGGNSNGPCVLPF 75
 DB 241 YSACTTDG---RSDGLPWCSTTANYP---TDPRFGCPSERLYTR---DGNADSKPCQFPF 292
 QY 76 TYNGRTFYSCTTEGRDGHLMCSTTSNYEQDKYSPC---TDHTVLVQTRGNSNGALCH 132
 DB 293 IFGGQSYSACTTDGRSDGRWCATTANYDRDKLFGCPTRADSTW---GGSAGELCV 348
 QY 133 FPFLLNNHNYTDTSGSRDNNMKCGTTONYDADQKFGCP-----MAAHE----- 178
 DB 349 FPFPLFGKEYSCTSGRSDGRMLWCATTSNFDSDKMKWGFCDQGYSLFLVAHAHFGHALG 408
 QY 179 -EICTNEGVMY 189
 DB 409 LDHSSVPEALMY 420

Search completed: November 28, 2003, 14:59:44
 Job time : 18 secs

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OM protein - protein search, using SW model

Run on: November 28, 2003, 14:59:11 ; Search time 44 Seconds

(Without alignments)
1237.346 Million cell updates/sec

Title: US-09-934-706-1

Sequence: 1 MAAYVQPPHPQPPYGHCV.....EVFTETPSQPNHPIQMLE 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2002	100.0	343	21	AA08505
2	2002	100.0	343	23	AB07961
3	1999	99.9	400	21	AA08509
4	1999	99.9	461	23	AB07965
5	1999	99.9	473	23	AB07965
6	1999	99.9	501	21	AA08508
7	1988	99.3	1173	22	ABG2275
8	1988	99.3	2265	22	AA08647
9	1988	99.3	2330	22	AA08646

10	1988	99.3	2355	22	AA08649	Human polypeptide
11	1988	99.3	2386	22	AA08648	Human polypeptide
12	1988	99.3	2446	21	AA05037	Human fibronectin
13	1984	99.1	2386	20	AA017353	Human fibronectin
14	1979	98.9	720	20	AA28914	Fibronectin protei
15	1979	98.9	2386	19	AA063171	Amino acid sequenc
16	1979	98.9	2477	20	AA099595	Human fibronectin
17	1978	98.8	2324	17	AA092778	Human fibronectin
18	1978	98.8	2324	23	AA032651	Human protein rela
19	1978	98.8	2324	23	AA074674	Human fibronectin
20	1978	98.8	2327	8	AA070373	Human fibronectin
21	1978	98.8	2328	22	AA068182	Fibronectin protei
22	1978	98.8	2328	24	AA041106	Human fibronectin
23	1978	98.8	2328	24	AB07486	Protein different
24	1978	98.8	2446	15	AA060021	Fibronectin-alpha.
25	1973	98.6	2327	12	AA015468	Human fibronectin
26	1959.5	97.9	2447	22	AA040432	Human polypeptide
27	1959.5	97.9	2447	22	AA040433	Human polypeptide
28	1959.5	97.9	2447	22	AA040434	Human polypeptide
29	1959.5	97.9	2447	22	AA040435	Human polypeptide
30	1950	97.4	2474	22	ABG22279	Novel human diagno
31	1859.5	92.9	660	20	AA028901	Human migration st
32	1326	66.2	285	23	AB06751	Collagen-binding e
33	1312	65.5	386	23	AB06750	Collagen-binding b
34	1311	65.5	228	23	AB06747	Human fibronectin
35	386	19.3	663	19	AA041227	Chicken matrix met
36	382.5	19.1	631	10	AA06143	Sequence of human
37	382.5	19.1	631	19	AA041226	Human mature matrl
38	382.5	19.1	644	22	AA020490	Human matrix metal
39	382.5	19.1	660	11	AA06420	Type IV collagenas
40	382.5	19.1	660	22	AA010431	Human matrix metal
41	382.5	19.1	660	22	AA084607	Amino acid sequenc
42	382.5	19.1	660	23	AB079413	Human matrix metal
43	382.5	19.1	660	23	AB090738	Human Tumor Endot
44	382.5	19.1	660	23	AB084348	Protein Wmp2 diffe
45	382.5	19.1	660	24	AB076322	Human matrix metal

ALIGNMENTS

RESULT 1	AA08505	AA08505 standard; Protein; 343 AA.
ID	AA08505	
AC	AA08505	
XX		
DT	20-DEC-2000	(first entry)
XX		
DE	Amino acid sequence of modified fibronectin collagen-binding domain.	
XX		
KW	Fibronectin; collagen-binding domain; sustained release; gene therapy;	
KW	physiologically active polypeptide; topical retention;	
KW	tissue regeneration.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "Met added for efficient expression"
XX		
PN	NO200049159-A1.	
XX		
PD	24-ANG-2000.	
XX		
PF	21-FEB-2000; 2000WO-JP00964.	
XX		
PR	19-FEB-1999; 99JP-0041913.	
PR	01-NOV-1999; 99JP-0311364.	
XX		
PA	(TERU) TERUMO CORP.	
XX		

PI Ishikawa T, Kiteajima T;
XX WPI; 2000-565375/52.
DR N-PSDB; AAA64263.
XX
PT Collagen-binding active polypeptide for use in an agent for enabling
topical retention or sustained release of a physiologically active
peptide or physiological activity-imparting agent comprises a
PT fibronectin peptide -
XX
PS Disclosure; Page 113-115; 135pp; English.
XX
CC The present sequence represents a modified fibronectin collagen-
binding domain. The protein is used to construct a collagen-binding
CC physiologically active polypeptide. This polypeptide comprises a
CC peptide from fibronectin ligated to a physiologically active peptide.
CC The polypeptides are used in an agent for enabling topical retention or
CC sustained release of a physiologically active peptide or physiological
CC activity-imparting agent. They may be used in gene therapy and in
CC tissue regeneration.
XX
SQ Sequence 343 AA;
Query Match 100.0%; Score 2002; DB 21; Length 343;
Best Local Similarity 100.0%; Pred. No. 3e-143;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPQPPYGHCVTDGAVYVSGMOMLKTQGNKOMLCTCLANGVSCQETAVTQ 60
Db 1 MAAVYQPPHPQPPYGHCVTDGAVYVSGMOMLKTQGNKOMLCTCLANGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPTFYNGRTFYSCTTEGRDGHLMCSTSNYEDQKYSFCTDHTVLVQ 120
Db 61 TYGNSNGEPCVLPTFYNGRTFYSCTTEGRDGHLMCSTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHYTDTCTSEGRDNMKWCGTTONYDADQKFGCPMAAHEI 180
Db 121 TRGNSNGALCHFPFLYNNHYTDTCTSEGRDNMKWCGTTONYDADQKFGCPMAAHEI 180
QY 181 CTTEGAVYRIGDQMDKOHDMGHMNRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVYVND 240
Db 181 CTTEGAVYRIGDQMDKOHDMGHMNRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIGDSMEKYVHGVRYQCYC 300
Db 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIGDSMEKYVHGVRYQCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQPNSHPIQWLE 343
Db 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQPNSHPIQWLE 343
RESULT 2
AB07961
ID ABB07961 standard; Protein; 343 AA.
XX
AC ABB07961;
XX
DT 12-AUG-2002 (first entry)
XX
DE Modified human fibronectin collagen-binding domain.
XX
KW Osteogenesis; drug delivery system; DDS; collagen; osteopathic; human;
fibronectin.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2002058485-A.
XX
PD 26-FEB-2002.
XX
FT 16-AUG-2000; 2000JP-0246744.

XX
PR 16-AUG-2000; 2000JP-0246744.
XX
PA (TERU) TERUMO CORP.
XX
DR WPI; 2002-438612/47.
DR N-PSDB; ABL41020.
XX
PT Novel osteogenesis stimulating fused protein having collagen avidity
used as an osteogenesis stimulator and a localizing agent -
XX
PS Disclosure; Page 17-18; 30pp; Japanese.
XX
CC The invention provides an osteogenesis stimulating fused protein (I) for
a drug delivery system (DDS) of osteogenic factor, having collagen
CC avidity and polypeptides homologous to collagen avidity domain or its
CC modified peptides. (I) is used for stimulation of osteogenesis, a
CC localizing agent and a slow releasing agent for a drug delivery system.
CC The present sequence represents a modified human fibronectin collagen-
binding domain.
XX
SQ Sequence 343 AA;
Query Match 100.0%; Score 2002; DB 23; Length 343;
Best Local Similarity 100.0%; Pred. No. 3e-143;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPQPPYGHCVTDGAVYVSGMOMLKTQGNKOMLCTCLANGVSCQETAVTQ 60
Db 1 MAAVYQPPHPQPPYGHCVTDGAVYVSGMOMLKTQGNKOMLCTCLANGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPTFYNGRTFYSCTTEGRDGHLMCSTSNYEDQKYSFCTDHTVLVQ 120
Db 61 TYGNSNGEPCVLPTFYNGRTFYSCTTEGRDGHLMCSTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHYTDTCTSEGRDNMKWCGTTONYDADQKFGCPMAAHEI 180
Db 121 TRGNSNGALCHFPFLYNNHYTDTCTSEGRDNMKWCGTTONYDADQKFGCPMAAHEI 180
QY 181 CTTEGAVYRIGDQMDKOHDMGHMNRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVYVND 240
Db 181 CTTEGAVYRIGDQMDKOHDMGHMNRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIGDSMEKYVHGVRYQCYC 300
Db 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIGDSMEKYVHGVRYQCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQPNSHPIQWLE 343
Db 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQPNSHPIQWLE 343
RESULT 3
AAB08509
ID AAB08509 standard; Protein; 400 AA.
XX
AC AAB08509;
XX
DT 20-DEC-2000 (first entry)
XX
DE Hybrid of fibronectin collagen-binding domain/epidermal growth factor.
XX
KW Fibronectin; collagen-binding domain; sustained release; gene therapy;
physiologically active polypeptide; topical retention; chimera;
KW tissue regeneration; epidermal growth factor.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 2..341 "human fibronectin collagen-binding domain"
FT Misc-difference 343..347

FT /note= "enterokinase recognition sequence"
FT 348.400
FT /note= "epidermal growth factor"
XX
XX WO200049159-A1.
XX
XX 24-AUG-2000.
XX
XX 21-FEB-2000; 2000WO-JP00964.
XX
XX 19-FEB-1999; 99JP-0041913.
XX 01-NOV-1999; 99JP-0311364.
XX
XX (TERU) TERUMO CORP.
XX
XX Ishikawa T, Kitajima T;
XX WPI; 2000-565375/52.
XX N-PSDB; AAA64271.
XX
XX Collagen-binding active polypeptide for use in an agent for enabling
PT topical retention or sustained release of a physiologically active
PT peptide or physiological activity-impacting agent comprises a
PT fibronectin peptide -
XX
XX Disclosure; Page 122-124; 135pp; English.
XX
XX The present sequence represents a hybrid polypeptide, comprising a
CC modified human fibronectin collagen-binding domain and a modified
CC human epidermal growth factor with an enterokinase recognition
CC sequence. The protein is representative of collagen-binding
CC physiologically active polypeptides of the invention. These
CC polypeptides comprise a peptide from fibronectin ligated to a
CC physiologically active peptide. The polypeptides are used in an
CC agent for enabling topical retention or sustained release of a
CC physiologically active peptide or physiological activity-impacting
CC agent. They may be used in gene therapy and in tissue regeneration.
XX
XX Sequence 400 AA;
SQ
Query Match 99.3%; Score 1999; DB 21; Length 400;
Best Local Similarity 99.7%; Pred. No. 6e-143;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPPPHCHCTDSDGVYVSGMOMLKTQGNKMLCTCLGNVSCQETAVTQ 60
DB 1 MAAYVQPPHPPPPHCHCTDSDGVYVSGMOMLKTQGNKMLCTCLGNVSCQETAVTQ 60
QY TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEBODKXSFCTDHTVLVQ 120
DB TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEBODKXSFCTDHTVLVQ 120
QY TYGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADOKFCFCPMAAHEE 180
DB TYGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADOKFCFCPMAAHEE 180
QY CTTEGMYMFIIGOMDKOHDMGHMMRCTCVNGRGEWTCIAYSQLRQCTIVDDITVND 240
DB CTTEGMYMFIIGOMDKOHDMGHMMRCTCVNGRGEWTCIAYSQLRQCTIVDDITVND 240
QY TFFKRHEEGLMCTCFGQGRGKMKDPVQCCDSEGTGYQIGDSNEKTVHGVRYCCYC 300
DB TFFKRHEEGLMCTCFGQGRGKMKDPVQCCDSEGTGYQIGDSNEKTVHGVRYCCYC 300
QY YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
DB YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
XX
XX RESULT 4
XX ABB07964 standard; Protein; 461 AA.

AC ABB07964;
XX
XX 12-AUG-2002 (first entry)
XX
XX Human fibronectin collagen-binding domain/BMP2 hybrid protein.
DE
XX Osteogenesis; drug delivery system; DSS; collagen; osteopathic; human;
XX fibronectin; BMP2; hybrid; fusion protein.
XX
XX Homo sapiens.
OS Synthetic.
XX JP2002058485-A.
XX
XX 26-FEB-2002.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX
XX (TERU) TERUMO CORP.
XX
XX WPI; 2002-438612/47.
XX N-PSDB; ABL41027.
XX
XX Novel osteogenesis stimulating fused protein having collagen avidity
PT used as an osteogenesis stimulator and a localizing agent -
XX
XX Disclosure; Page 23-25; 30pp; Japanese.
XX
XX The invention provides an osteogenesis stimulating fused protein (I) for
CC a drug delivery system (DSS) of osteogenic factor, having collagen
CC avidity and polypeptides homologous to collagen avidity domain or its
CC modified peptides. (I) is used for stimulation of osteogenesis, a
CC localized agent and a slow releasing agent for a drug delivery system.
CC The present sequence represents a human fibronectin collagen-binding
CC domain/human BMP2 hybrid protein.
XX
XX Sequence 461 AA;
SQ
Query Match 99.3%; Score 1999; DB 23; Length 461;
Best Local Similarity 99.7%; Pred. No. 7e-143;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPPPHCHCTDSDGVYVSGMOMLKTQGNKMLCTCLGNVSCQETAVTQ 60
DB 1 MAAYVQPPHPPPPHCHCTDSDGVYVSGMOMLKTQGNKMLCTCLGNVSCQETAVTQ 60
QY TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEBODKXSFCTDHTVLVQ 120
DB TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEBODKXSFCTDHTVLVQ 120
QY TYGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADOKFCFCPMAAHEE 180
DB TYGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADOKFCFCPMAAHEE 180
QY CTTEGMYMFIIGOMDKOHDMGHMMRCTCVNGRGEWTCIAYSQLRQCTIVDDITVND 240
DB CTTEGMYMFIIGOMDKOHDMGHMMRCTCVNGRGEWTCIAYSQLRQCTIVDDITVND 240
QY TFFKRHEEGLMCTCFGQGRGKMKDPVQCCDSEGTGYQIGDSNEKTVHGVRYCCYC 300
DB TFFKRHEEGLMCTCFGQGRGKMKDPVQCCDSEGTGYQIGDSNEKTVHGVRYCCYC 300
QY YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
DB YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
XX
XX RESULT 5
XX ABB07965 standard; Protein; 473 AA.

AC AAB07965;
XX 12-AUG-2002 (first entry)
XX Human fibronectin collagen-binding domain/BMP7 hybrid protein.
DE
XX Osteogenesis; drug delivery system; DDS; collagen; osteopathic; human;
XX fibronectin; BMP7; hybrid; fusion protein.
XX Homo sapiens.
OS Synthetic.
XX JP2002058485-A.
XX 26-FEB-2002.
XX 16-AUG-2000; 2000JP-0246744.
XX 16-AUG-2000; 2000JP-0246744.
XX (TERU) TERUMO CORP.
XX WPI: 2002-438612/47.
XX N-PSDB; ABL41028.
XX Novel osteogenesis stimulating fused protein having collagen avidity
XX used as an osteogenesis stimulator and a localizing agent -
XX
XX Disclosure; Page 26-28; 30pp; Japanese.
XX
XX The invention provides an osteogenesis stimulating fused protein (1) for
XX a drug delivery system (DDS) of osteogenic factor, having collagen
XX avidity and polypeptides homologous to collagen avidity domain or its
XX modified peptide. (1) is used for stimulation of osteogenesis, a
XX localizing agent and a slow releasing agent for a drug delivery system.
XX The present sequence represents a human fibronectin collagen-binding
XX domain/human BMP7 hybrid protein.
XX
XX Sequence 473 AA;
SQ
Query Match 99.9%; Score 1999; DB 23; Length 473;
Best Local Similarity 99.7%; Pred. No. 7.2e-143; Indels 0; Gaps 0;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPPPYGHCVTDGSGVYVSVGMQMLKTQGNKQMLCTCLNGVSCQETAVTQ 60
DB 1 MAAVYQPPHPPPPYGHCVTDGSGVYVSVGMQMLKTQGNKQMLCTCLNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDTSGRRDNMKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDTSGRRDNMKCGTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVYRIGDQDKDGMHMRCTCVNGRGEWTCLAYSQLRDQCIYDDITVYVND 240
DB 181 CTTEGVYRIGDQDKDGMHMRCTCVNGRGEWTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHLNCTCFGQGRGWKCDPVDCQDSESTGFYQIGDSWEKYYHGVAYCYC 300
DB 241 TFHRRHEGHLNCTCFGQGRGWKCDPVDCQDSESTGFYQIGDSWEKYYHGVAYCYC 300
QY 301 YGRGIGEMHCOPLQTPSSSGPVEVITETPSQPSHPIOMLE 343
DB 301 YGRGIGEMHCOPLQTPSSSGPVEVITETPSQPSHPIOMLE 343
RESULT 6
AAB08508
ID. AAB08508 standard; Protein. 501 AA.
XX

AC AAB08508;
XX 20-DEC-2000 (first entry)
XX Hybrid of fibronectin collagen-binding domain/fibroblast growth factor.
DE
XX Fibronectin; collagen-binding domain; sustained release; gene therapy;
XX physiologically active polypeptide; topical retention; chimera;
XX tissue regeneration; fibroblast growth factor.
XX Chimeric - Homo sapiens.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 2..341
XX Protein /note= "human fibronectin collagen-binding domain"
XX FT /note= "enterokinase recognition sequence"
XX FT /note= "348..501
XX FT Protein /note= "fibroblast growth factor"
XX
XX WO200049159-A1.
XX 24-AUG-2000.
XX 21-FEB-2000; 2000WO-JP00964.
XX 19-FEB-1999; 99JP-0041913.
XX 01-NOV-1999; 99JP-0311364.
XX (TERU) TERUMO CORP.
XX
XX Ishikawa T, Kitajima T;
XX WPI: 2000-565375/52.
XX N-PSDB; AAA64270.
XX
XX Collagen-binding active polypeptide for use in an agent for enabling
XX topical retention or sustained release of a physiologically active
XX peptide or physiological activity-imparting agent comprises a
XX fibronectin peptide -
XX
XX Disclosure; Page 118-121; 135pp; English.
XX
XX The present sequence represents a hybrid polypeptide, comprising a
XX modified human fibronectin collagen-binding domain and a modified
XX human fibroblast growth factor with an enterokinase recognition
XX sequence. The protein is representative of collagen-binding
XX physiologically active polypeptides of the invention. These
XX polypeptides comprise a peptide from fibronectin ligated to a
XX physiologically active peptide. The polypeptides are used in an
XX agent for enabling topical retention or sustained release of a
XX physiologically active peptide or physiological activity-imparting
XX agent. They may be used in gene therapy and in tissue regeneration.
XX
XX Sequence 501 AA;
SQ
Query Match 99.9%; Score 1999; DB 21; Length 501;
Best Local Similarity 99.7%; Pred. No. 7.7e-143; Indels 0; Gaps 0;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPPPYGHCVTDGSGVYVSVGMQMLKTQGNKQMLCTCLNGVSCQETAVTQ 60
DB 1 MAAVYQPPHPPPPYGHCVTDGSGVYVSVGMQMLKTQGNKQMLCTCLNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDTSGRRDNMKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDTSGRRDNMKCGTTONYADQKFGFCPMAAHEI 180

QY 181 CTNNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIYDDITYNVND 240
DB 181 CTNNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIYDDITYNVND 240
QY 241 TFKRHEEGMLNCTCGQGRGKWKCDPVQCCDSSETGYQIGDSWEKTVHGVRYCCY 300
DB 241 TFKRHEEGMLNCTCGQGRGKWKCDPVQCCDSSETGYQIGDSWEKTVHGVRYCCY 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSOPNSHIOMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSOPNSHIOMLE 343
RESULT 7
ABG22275
ID ABG22275 standard; Protein; 1173 AA.
XX ABG22275;
AC
XX
XX 18-FEB-2002 (first entry)
DE Novel human diagnostic protein #22266.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS86462.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 20; SEQ ID NO 52634; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG0010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SEQ Sequence 1173 AA;
Query Match 99.3%; Score 1988; DB 22; Length 1173;
Best Local Similarity 100.0%; Pred. No. 1,4e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAYVQPPHQPPEYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 245 AAYVQPPHQPPEYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 304
QY 62 YGNSNGEPCVLPFTYNGRFFYCTTGRDGHLMCTSNYBDDQKYSFCTDHTVLVQT 121
DB 305 YGNSNGEPCVLPFTYNGRFFYCTTGRDGHLMCTSNYBDDQKYSFCTDHTVLVQT 364
QY 122 RGNNSGALCHFPFLVNNHNYTCTSGRDNMKCGTTONYADQKFGCPMAAHEIC 181
DB 365 RGNNSGALCHFPFLVNNHNYTCTSGRDNMKCGTTONYADQKFGCPMAAHEIC 424
QY 182 TTNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIYDDITYNVNDT 241
DB 425 TTNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIYDDITYNVNDT 484
QY 242 FHKRHEEGMLNCTCGQGRGKWKCDPVQCCDSSETGYQIGDSWEKTVHGVRYCCY 301
DB 485 FHKRHEEGMLNCTCGQGRGKWKCDPVQCCDSSETGYQIGDSWEKTVHGVRYCCY 544
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFTTETPSOPNSHIOM 341
DB 545 GRGIGEMHCOPLOTYPSSSGPVEVFTTETPSOPNSHIOM 584
RESULT 8
AAM38647
ID AAM38647 standard; Protein; 2265 AA.
XX
XX AAM38647;
XX
XX 22-OCT-2001 (first entry)
XX
XX
DE Human polypeptide SEQ ID NO 1792.
XX
XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX
OS Homo sapiens.
XX
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AAI57803.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS Example 3; SEQ ID NO 1792; 10078bp; English.
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA157798-AA161369) with nootropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2265 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2265;
Best Local Similarity 100.0%; Pred. No. 2.9e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQPHPPPPYGHCVTDSGVVYSGVMQMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 61
DB 291 AAVYQPHPPPPYGHCVTDSGVVYSGVMQMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 350
QY 62 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNVEEDOKXSFCTDHTLVYTQT 121
DB 351 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNVEEDOKXSFCTDHTLVYTQT 410
QY 122 RGSNSGALCHFPFLYNNHNTDCTSEGRDMMKCGTTONYVADADOKRFGCPMAAHEIC 181
DB 411 RGSNSGALCHFPFLYNNHNTDCTSEGRDMMKCGTTONYVADADOKRFGCPMAAHEIC 470
QY 182 TTNGVWYRIGDQMDKQHDGMHMRCTCVGNGRGEMTICIASQLRDCIYVDITVYVNDT 241
DB 471 TTNGVWYRIGDQMDKQHDGMHMRCTCVGNGRGEMTICIASQLRDCIYVDITVYVNDT 530
QY 242 FHKRHEBGMHNCCTCFGGRGRWKCDPVDOCDSETGFYQIGSWEXYVGVRYQCYCY 301
DB 531 FHKRHEBGMHNCCTCFGGRGRWKCDPVDOCDSETGFYQIGSWEXYVGVRYQCYCY 590
QY 302 GRGIGEMHCOPLOQTYPSSSGPEVEFITTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLOQTYPSSSGPEVEFITTETPSQPNSHPIOW 630
RESULT 9
ID AA157798 standard; Protein; 2330 AA.
XX
XX
AC AA157798;
XX
XX
DE 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 1791.
XX
XX Human, nootropic, immunosuppressant, cytoskeletal, gene therapy, cancer;
XX peripheral nervous system, neuropathy, central nervous system, CNS;
XX Alzheimer's, Parkinson's disease, Huntington's disease, haemostatic;
XX amyotrophic lateral sclerosis, Shy-Drager Syndrome, chemotactic;
XX chemokinetic, thrombolytic, drug screening, arthritis, inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX

FN WO200153312-A1.
XX
XX
PD 26-JUL-2001.
XX
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX
PA (HSE-) HSEQ INC.
XX
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;
PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;
XX
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AA157802.
XX
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS Example 3; SEQ ID NO 1791; 10078bp; English.
XX
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA157798-AA161369) with nootropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2330 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2330;
Best Local Similarity 100.0%; Pred. No. 3e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQPHPPPPYGHCVTDSGVVYSGVMQMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 61
DB 291 AAVYQPHPPPPYGHCVTDSGVVYSGVMQMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 350
QY 62 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNVEEDOKXSFCTDHTLVYTQT 121
DB 351 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNVEEDOKXSFCTDHTLVYTQT 410
QY 122 RGSNSGALCHFPFLYNNHNTDCTSEGRDMMKCGTTONYVADADOKRFGCPMAAHEIC 181
DB 411 RGSNSGALCHFPFLYNNHNTDCTSEGRDMMKCGTTONYVADADOKRFGCPMAAHEIC 470
QY 182 TTNGVWYRIGDQMDKQHDGMHMRCTCVGNGRGEMTICIASQLRDCIYVDITVYVNDT 241
DB 471 TTNGVWYRIGDQMDKQHDGMHMRCTCVGNGRGEMTICIASQLRDCIYVDITVYVNDT 530
QY 242 FHKRHEBGMHNCCTCFGGRGRWKCDPVDOCDSETGFYQIGSWEXYVGVRYQCYCY 301
DB 531 FHKRHEBGMHNCCTCFGGRGRWKCDPVDOCDSETGFYQIGSWEXYVGVRYQCYCY 590
QY 302 GRGIGEMHCOPLOQTYPSSSGPEVEFITTETPSQPNSHPIOW 341

DB 591 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSPQNSHPIDW 630

RESULT 10

ID AAM38649 standard; Protein; 2355 AA.

AC AAM38649;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 1794.

XX Human; nocrotropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokine; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

PI WPI, 2001-442253/47.

DR N-PSDB; AAI57805.

DR Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX Example 3; SEQ ID NO 1794; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and

XX the encoded polypeptides (AAM38642-AA42213) with nocrotropic,

XX immunosuppressant and cyostatic activity. The polynucleotides are useful

XX in gene therapy. A composition containing a polypeptide or polynucleotide

XX of the invention may be used to treat diseases of the peripheral nervous

XX system, such as peripheral nervous injuries, peripheral neuropathy and

XX localised neuropathies and central nervous system diseases, such as

XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

XX utilisation of the activities such as: Immune system suppression,

XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,

XX C.N.S disorders.

XX Note: The sequence data for this patent did not form part of the printed

XX specification.

XX Sequence 2355 AA;

XX Query Match 99.3%; Score 1988; DB 22; Length 2355;

XX Best Local Similarity 100.0%; Pred. No. 3e-141;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVYQPPHPPPPPYCHCTDSDGVVYSVGMOMLKTQGNOMLCTCLGNGVSCQETAVTQ 61

DB 291 AAVYQPPHPPPPPYCHCTDSDGVVYSVGMOMLKTQGNOMLCTCLGNGVSCQETAVTQ 350

QY 62 YGNSNGEPCVLPFTYNGRTFYSCTEGRODGLMCSSTSNYEQDQKSFCTDHTLVQT 121

DB 351 YGNSNGEPCVLPFTYNGRTFYSCTEGRODGLMCSSTSNYEQDQKSFCTDHTLVQT 410

QY 122 RGNNSGALCHPPELYNNHNYTDCSEGRDMMKCGTTQNDADQKFGCPMAAHEIC 181

DB 411 RGNNSGALCHPPELYNNHNYTDCSEGRDMMKCGTTQNDADQKFGCPMAAHEIC 470

QY 182 TTNEGMYRIRIGQMDQHMGMHMRCTCVNGRGENTCLAYSRLRQCTVDITVNDT 241

DB 471 TTNEGMYRIRIGQMDQHMGMHMRCTCVNGRGENTCLAYSRLRQCTVDITVNDT 530

QY 242 FHKRHEGMLNCTCFGQGRGKCDPVQOCDSFTGTFYQIGDSWEKTVHGVYOCYCY 301

DB 531 FHKRHEGMLNCTCFGQGRGKCDPVQOCDSFTGTFYQIGDSWEKTVHGVYOCYCY 590

QY 302 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSPQNSHPIDW 341

DB 591 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSPQNSHPIDW 630

RESULT 11

ID AAM38648 standard; Protein; 2386 AA.

AC AAM38648;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 1793.

XX Human; nocrotropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS;

XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

XX chemokine; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

PI WPI, 2001-442253/47.

DR N-PSDB; AAI57804.

DR Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

PS Example 3; SEQ ID NO 1793; 10078bp; English.
XX The invention relates to human nucleic acids (AA15798-AA161369) and
XX the encoded polypeptides (AA038642-AA042213) with nocotropic.
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX
SQ Sequence 2386 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2386;
Best Local Similarity 100.0%; Pred. No. 3,1e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQOPHPQPPYGHGCVTDGIVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHGCVTDGIVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGGSNSNEPCVLPPTYNAGRTFYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 121
DB 351 YGGSNSNEPCVLPPTYNAGRTFYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSNGALCHFPPLNNHNTTDCSTSEGRDNMKCGTTONYDADOKRFGFPMANHEBIC 181
DB 411 RGSNSNGALCHFPPLNNHNTTDCSTSEGRDNMKCGTTONYDADOKRFGFPMANHEBIC 470
QY 182 TTNEGVMYRIGDQDKDHDMHMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 241
DB 471 TTNEGVMYRIGDQDKDHDMHMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 530
QY 242 FHKHSEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGDSWEKYVAGVAYQCYCY 301
DB 531 FHKHSEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGDSWEKYVAGVAYQCYCY 590
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 630
RESULT 12
AAB50377
ID AAB50377 standard; Protein; 2446 AA.
AC AAB50377;
XX
XX 12-MAR-2001 (first entry)
XX
XX Human fibronectin.
XX
XX Human; FN; fibronectin; prostate cancer; biallelic marker; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2000058509-A2.
XX
XX 05-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-1B00431.
XX
XX 29-MAR-1999; 99US-0126780.
XX
XX (GEST) GENSET.
XX

XX
XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;
PI WPI: 2000-594647/56.
DR N-PSDB; AAC89889.
XX
XX Fibronectin polynucleotide and polypeptide sequences, useful for
PT determining the predisposition of individuals to cancer, such as
PT prostate cancer -
XX
PS Claim 4; Page 185-190; 208pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC or purified recombinant polynucleotide comprising a contiguous span of at
CC least 12 nucleotides of a fibronectin (FN) gene. The methods and
CC sequences are useful for determining the predisposition of individuals to
CC cancer such as prostate cancer and for the prognosis/detection of an
CC eventual treatment response to therapeutic agents acting against prostate
CC cancer. Biallelic markers allow association studies to be performed
CC to identify genes involved in complex traits.
XX
XX
SQ Sequence 2446 AA;
Query Match 99.3%; Score 1988; DB 21; Length 2446;
Best Local Similarity 100.0%; Pred. No. 3,2e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQOPHPQPPYGHGCVTDGIVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHGCVTDGIVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGGSNSNEPCVLPPTYNAGRTFYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 121
DB 351 YGGSNSNEPCVLPPTYNAGRTFYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSNGALCHFPPLNNHNTTDCSTSEGRDNMKCGTTONYDADOKRFGFPMANHEBIC 181
DB 411 RGSNSNGALCHFPPLNNHNTTDCSTSEGRDNMKCGTTONYDADOKRFGFPMANHEBIC 470
QY 182 TTNEGVMYRIGDQDKDHDMHMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 241
DB 471 TTNEGVMYRIGDQDKDHDMHMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 530
QY 242 FHKHSEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGDSWEKYVAGVAYQCYCY 301
DB 531 FHKHSEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGDSWEKYVAGVAYQCYCY 590
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 630
RESULT 13
AA017353
ID AA017353 standard; protein; 2386 AA.
AC AA017353;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human fibronectin.
XX
XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;
KW platelet derived growth factor receptor alpha; laminin M chain;
KW subtilisin like protein PACE4; nidogen.
XX
XX Homo sapiens.
XX
XX EP1191107-A2.
XX

PD 27-MAR-2002.
 XX
 PF 21-AUG-2001; 2001EP-0250300.
 XX
 PR 25-SEP-2000; 2000DE-1048633.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Hess-stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E,
 PI Regidor P, Scotti S;
 XX WPI; 2002-317413/36.
 DR
 XX
 XX In vitro diagnosis and monitoring of endometriosis, comprises
 PT detecting reduced expression of specific gene products, e.g. from the
 PT fibronectin gene -
 XX
 PS Claim 1; Page 9-10; 21pp; German.
 XX
 CC The present invention relates to a method for the in vitro diagnosis of
 CC endometriosis by determining the amount of gene product from at least one
 CC specific gene in a patient sample and comparing this with the amount of
 CC gene product in a control sample. A reduced level is indicative of
 CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
 CC transmembrane receptor PK7, collagen type XVIII alpha 1,
 CC platelet derived growth factor receptor alpha, laminin M chain,
 CC subfollin like protein PAC4 or nidogen. The method is useful for
 CC initial diagnosis of endometriosis, and also for monitoring progress and
 CC treatment of the disease. The present sequence is human fibronectin.
 CC
 SQ Sequence 2386 AA;

Query Match 99.1%; Score 1984; DB 23; Length 2386;
 Best Local Similarity 99.7%; Pred. No. 6.2e-141;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAYQOPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
 DB 291 AAYQOPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 350
 QY 62 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSFCTDHTVLVQT 121
 DB 351 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSFCTDHTVLVQT 410
 QY 122 RGNNSGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTNYADOKFGFCPMAAHEIC 181
 DB 411 QGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTNYADOKFGFCPMAAHEIC 470
 QY 182 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGNGRGEWTCIAYSQLRDQCIYDDITVYNDT 241
 DB 471 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGNGRGEWTCIAYSQLRDQCIYDDITVYNDT 530
 QY 242 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYVHGVRYOCYCY 301
 DB 531 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYVHGVRYOCYCY 590
 QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFITETPSQPNSHDIOW 341
 DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFITETPSQPNSHDIOW 630

RESULT 14
 AAY28914
 ID AAY28914 standard; Protein; 720 AA.
 XX
 AC AAY28914;
 XX
 XX 21-SEP-1999 (first entry)
 XX
 DE Fibronectin protein sequence.
 XX

KW Migration stimulatory factor; MSF; cell migration; modulation; human;
 KW wound healing; scarring; MSF-alpha; epitope; fibronectin.
 XX
 OS Homo sapiens.
 XX
 PN W09931233-A1.
 XX
 XX 24-JUN-1999.
 PD
 XX
 PF 15-DEC-1998; 98WO-GB03766.
 XX
 PR 16-DEC-1997; 97GB-0026539.
 XX
 XX (UYDU-) UNIV DUNDEE.
 PA
 PI Schor AM, Schor SL;
 XX WPI; 1999-430039/36.
 DR
 XX
 XX Proteins with cell migration stimulatory activity used in treating
 PT wound and preventing scarring
 PT
 XX
 PS Disclosure; Fig 2; 86pp; English.
 XX
 CC The invention provides a human migration stimulatory factor (MSF)
 CC protein. Host cells containing a replicable vector comprising the MSF
 CC encoding nucleic acid can be used for the recombinant production of the
 CC protein. The polypeptide can be used for modulating cell migration,
 CC healing a wound and for preventing scarring. The present sequence
 CC represents the human fibronectin.
 CC
 SQ Sequence 720 AA;

Query Match 98.9%; Score 1979; DB 20; Length 720;
 Best Local Similarity 99.4%; Pred. No. 3.8e-141;
 Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AAYQOPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
 DB 309 AAYQOPHPQPPYGHCVTDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 368
 QY 62 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSFCTDHTVLVQT 121
 DB 369 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSFCTDHTVLVQT 428
 QY 122 RGNNSGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTNYADOKFGFCPMAAHEIC 181
 DB 429 QGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTNYADOKFGFCPMAAHEIC 488
 QY 182 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGNGRGEWTCIAYSQLRDQCIYDDITVYNDT 241
 DB 489 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGNGRGEWTCIAYSQLRDQCIYDDITVYNDT 548
 QY 242 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYVHGVRYOCYCY 301
 DB 549 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYVHGVRYOCYCY 608
 QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFITETPSQPNSHDIOW 341
 DB 609 GRGIGEMHCOPLQTYPSSSGPVEVFITETPSQPNSHDIOW 648

RESULT 15
 AAM63171
 ID AAM63171 standard; peptide; 2386 AA.
 XX
 AC AAM63171;
 XX
 XX 27-OCT-1998 (first entry)
 XX
 DE Amino acid sequence of fibronectin.
 DE Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
 XX

KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KW inflammatory skin condition; fibronectin.

OS Mus sp.

XX W09833812-A1.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01865.

XX 05-FEB-1997; 97US-0037090.

XX (BGMH) BRIGHAM & WOMENS HOSPITAL.

XX Huang C, Stevens RL;

XX WPI; 1998-437390/37.

PT Tryptase-6 complex inhibitory peptides - used to treat mast
 cell-mediated inflammatory disorders e.g. asthma

PS Disclosure; Pages 36-42; 69pp; English.

CC This is the amino acid sequence of fibronectin. The tryptase-6 complex
 CC inhibitory peptides of the invention comprise the sequence of a fragment
 CC of the fibronectin (residues 1351-1356). Sequences shown in AAM63160 to
 CC AAM63169 represent mouse mast cell protease (mMCP-6) inhibitory
 CC peptides. These peptides which are tryptase-6 complex inhibitors, can be
 CC used for treating a mast cell-mediated inflammatory disorder. The
 CC inhibitors can be used to treat inflammatory disorders including asthma,
 CC allergic rhinitis, urticaria and antioedema, eczematous dermatitis
 CC (atopic dermatitis), anaphylaxis, hyperproliferative skin disease, peptic
 CC ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory
 CC skin conditions.

XX SQ Sequence 2386 AA;

Query Match 98.9%; Score 1979; DB 19; Length 2386;

Best Local Similarity 99.4%; Pred. No. 1.5e-140; Indels 0; Gaps 0;

Matches 338; Conservative 1; Mismatches 1;

QY 2 AAVYQPPHPPPPYGHCVTDGVSVMQMLKTQGNKMLCTCLGNGVSCQETAVYQT 61
 DB 291 AAVYQPPHPPPPYGHCVTDGVSVMQMLKTQGNKMLCTCLGNGVSCQETAVYQT 350
 QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRDGHLWCSTTSNVEDOKYSFCTDHTVLVQT 121
 DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRDGHLWCSTTSNVEDOKYSFCTDHTVLVQT 410
 QY 122 RGNSNGALCHFPPLYNHNNTDCTSEGRNDMMKCGTTQNYVDADOKGFCPMAHEIC 181
 DB 411 QGNSNGALCHFPPLYNHNNTDCTSEGRNDMMKCGTTQNYVDADOKGFCPMAHEIC 470
 QY 182 TTNEGVMYRIQDQDKDQKDHMMKCTCVGNGRGEMTCIAYSQLRDQCIYDDITVNDT 241
 DB 471 TTNEGVMYRIQDQDKDQKDHMMKCTCVGNGRGEMTCIAYSQLRDQCIYDDITVNDT 530
 QY 242 FHKHBEHGMILNCTCFQGGGRMKCDPVDCQDSFTGYQIGDSEKRYHGVRYQCYCY 301
 DB 531 FHKHBEHGMILNCTCFQGGGRMKCDPVDCQDSFTGYQIGDSEKRYHGVRYQCYCY 590
 QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFITTPSQPNSHPIQW 341
 DB 591 GRGIGEMHCOPLOTYPSSSGPVEVFITTPSQPNSHPIQW 630

Search completed: November 28, 2003, 15:00:41
 Job time : 46 secs